APPENDIX A. STATISTICAL SUPPORT FOR PROPOSED SURFACE SEDIMENT AND TISSUE SAMPLING DESIGNS

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Acronyms

95UCL	95% upper confidence limit for the mean
COC	contaminant of concern
cPAH	carcinogenic polycyclic aromatic hydrocarbon
CLT	Central Limit Theorem
CV	coefficient of variation
DL	detection limit
dw	dry weight
EAA	early action area
FS	feasibility study
GOF	goodness-of-fit
LDW	Lower Duwamish Waterway
MNR	monitored natural recovery
PCB	polychlorinated biphenyl
ppb	parts per billion
RAO	remedial action objective
RI	remedial investigation
RM	river mile
RME	relative margin of error
ROD	Record of Decision
SD	standard deviation
SWAC	spatially weighted average concentration
TEQ	toxic equivalent
TTL	target tissue level
ww	wet weight

1 Introduction

A statistical evaluation was conducted to support the sampling design for the collection of surface sediment (0–10 cm) and fish and crab tissue. The remedial investigation/feasibility study (RI/FS) dataset for sediment and tissue was used to derive variance estimates that were used to estimate the appropriate number of samples of each.

1.1 SURFACE SEDIMENT (0–10 CM)

To develop the surface sediment sampling design, data from monitored natural recovery (MNR) areas identified in Record of Decision (ROD) Figure 18[1] (EPA 2014) were used to estimate the magnitude and patterns of variability expected in the Lower Duwamish Waterway (LDW) following active remediation.[2]

The targeted relative margin of error (RME) for the site-wide mean concentration for surface sediments (0–10 cm) in the LDW is 25%, wherein the RME is calculated as the width of the 95% upper confidence limit for the mean (95UCL) as a percent of the mean.[3] The sampling objective to estimate the site-wide mean with a RME of 25% can be met most cost-effectively through the use of composite samples. The baseline surface sediment (0–10 cm) sampling design will provide an efficient estimate of the 95UCL for cleanup goals for remedial action objectives (RAOs) 1, 2, and 4.[4]

A spatially balanced design has been developed that includes the collection of a single random sample within each of 100 grid cells of equal area distributed throughout the river. Twenty composite samples are then constructed from groups of five individual samples for analysis. This approach avoids bias and spatial clustering of samples so that the arithmetic mean of the observations is, in effect, a spatially weighted average concentration (SWAC), because equal spatial weighting is intrinsic to the design.

In future years of site-wide monitoring for RAOs 1, 2, and 4, the boundaries of the sampling grid cells and the compositing scheme among grid cells will remain constant. The sample locations will be randomly placed within each grid cell for each monitoring event, providing an unbiased characterization of each grid cell at that point in time. With this sampling design, the baseline and each future survey will maintain the same

[1] ROD Figure 18 is titled *Selected remedy*.
[2] It is acknowledged that baseline sediment chemistry variability will likely be greater than the variability estimated from the MNR dataset, and may be skewed rather than symmetric (i.e., follow a gamma distribution rather than a normal distribution).
[3] See Section 5.1 for more details.
[4] RAO 1 is related to consumption of resident seafood (human health), RAO 4 is related to high-trophic-level ecological risks (river otter), and RAO 2 is related to direct contact (human health) from netfishing (using 0–10-cm sediment samples throughout the LDW) and clamming and beach play (using 0–45-cm sediment sampling in specified areas).

connection to a spatial area within the site (e.g., composite sample No. 1 will always provide an unbiased estimate of the mean of the spatial area defined by grid cells 1 through 5). In this way, a robust site-wide 95UCL can be calculated for each sampling event.

1.2 FISH AND CRAB TISSUE

The fish and crab tissue sampling effort is designed to estimate the LDW-wide 95UCL concentrations for comparison to target tissue levels (TTLs) related to RAO 1 (ROD Table 21[5] (EPA 2014)). The targeted RME for the site-wide mean concentration for fish and crab tissues in the LDW is 25%, wherein the RME is calculated as the width of the LDW-wide 95UCL as a percent of the mean.[6]

To develop the fish and crab tissue sampling design, past data from several LDW tissue sampling efforts (primarily the 2007 RI/FS dataset with additional information for Dungeness crab provided by sample results from 2004 and 2005 (Windward 2010)) were evaluated. Distributional characteristics of the individual tissue concentrations and site-wide patterns in the mean concentrations were used to identify the best statistical model to identify the sample sizes expected to achieve the targeted RME.

The recommended design includes dividing the LDW into two reaches with four subreaches and creating composite samples of each tissue type within each reach. The reach designations are based on concentration patterns observed in previous tissue data and, where fishing occurs for resident species, per the fishers study (Windward 2016).

1.3 APPENDIX ORGANIZATION

The remainder of this appendix is organized as follows:

- Section 2 summarizes the data that were used to estimate post-remediation variances, which are used to plot the relationship between sample size and RME. The data from surface sediments (0–10 cm) and fish and crab tissues were extracted from the RI sediment and tissue datasets (Windward 2010).
- Section 3 presents the methods used to make meaningful estimates from the previous datasets to predict patterns of variability for baseline and future monitoring and to develop optimal sampling designs. Sampling methods, sampling frames (i.e., areas targeted for sampling), and sampling objectives are some of the ways in which the RI datasets differed substantially from baseline and future LDW sampling efforts. The statistical approach used in this appendix to extract summary statistics relevant to the development of the baseline sampling design are detailed for surface sediments (Section 3.1) and fish and crab tissues (Section 3.2).

[5] ROD Table 21 is titled *LDW resident fish and shellfish target tissue concentrations.*
[6] See Section 5.2 for more details.

- Section 4 presents the results from the methods outlined in Section 3, including a summary of the distributional characteristics and estimates of variability for sediments (Section 4.1) and fish and crab tissues (Section 4.2).
- Section 5 presents methods for calculating the compliance metric (95UCL) for surface sediments and fish and crab tissues, intertidal sediments (0–45 cm) for direct contact during beach play and clamming scenarios, and clam tissues.
- Section 6 discusses the conclusions regarding sampling variability for the study designs considered herein and makes final recommendations for sediment and tissue baseline and future monitoring.

2 Data Used in the Analysis

2.1 Surface Sediments (0–10 cm)

Surface sediment data from MNR areas (as depicted in ROD Figure 18 and Map B-1 of this appendix) within the RI/FS dataset were used in this evaluation. Data from MNR areas were selected because they provided the best surrogates for data variability likely to exist following active remediation in the LDW.[7] Results for total PCBs (sum of Aroclors]), carcinogenic polycyclic aromatic hydrocarbon (cPAH) toxic equivalent (TEQ), and arsenic were evaluated.[8]

A summary of the data for each contaminant of concern (COC) by river mile (RM) segment is presented in Table 1. The three COCs were mostly detected in this dataset (i.e., 88% of the PCB samples had detected concentrations and 95% of the cPAH and arsenic samples had detected concentrations). The data for total PCBs were the most abundant, with sample counts within each segment ranging from 8 to 103 for total PCBs and from 4 to 61 for both cPAH and arsenic. Sample locations within segments were clustered to varying degrees throughout the site; nearest neighbors were less than 50 ft apart in all but one segment for total PCBs, and in all but four segments for cPAH and arsenic.

[7] The only data that were excluded from the MNR area dataset were perimeter samples associated with early action areas (EAAs) (Terminal 117, Slip 4, and Duwamish Diagonal) that were collected prior to remediation and had polychlorinated biphenyl (PCB) concentrations greater than 400 µg/kg dry weight (dw).

[8] The sums of PCB Aroclors and cPAH TEQ were calculated using the LDW RI/FS data management rules. The dioxin/furan data are limited and thus no evaluation has been conducted for dioxin/furan TEQs.

Table 1. Summary of surface sediment (0–10 cm) data from MNR areas within the RI/FS dataset used to evaluate statistical properties of proposed study designs

RM Segment[a]	Total PCBs (ug/kg, dw)				cPAH TEQ (ug/kg, dw)			Arsenic (mg/kg, dw)		
	Total N	No. Non-detects	Concentration Range[b]	Min. Distance Between Samples (ft)	Total N	No. Non-detects	Min. Distance Between Samples (ft)	Total N	No. Non-detects	Min. Distance Between Samples (ft)
[0,0.1]	16	1	[8.4-250]	21	14	1	21	14	0	21
(0.1,0.3]	17	3	[3.1-191]	1	14	1	1	14	0	1
(0.3,0.5]	16	0	[7.0-222]	46	13	0	97	13	1	97
(0.5,0.6]	18	4	[0.4-341]	1	21	2	1	21	3	1
(0.6,0.7]	16	2	[2.6-340]	46	11	0	46	11	0	46
(0.7,0.9]	19	1	[4-196]	58	11	0	87	11	0	87
(0.9,1]	8	0	[51-240]	20	4	0	210	4	0	210
(1,1.2]	16	1	[4-302]	12	12	0	62	12	0	62
(1.2,1.4]	13	0	[66-290]	11	10	0	11	10	0	11
(1.4,1.6]	17	2	[10-340]	25	13	0	25	15	0	25
(1.6,1.8]	30	6	[9.5-270]	11	22	0	11	25	0	11
(1.8,2]	16	1	[9.5-260]	17	13	0	17	14	0	17
(2,2.1]	13	0	[38-296]	37	10	0	49	10	0	49
(2.1,2.7]	32	1	[10-204]	35	21	2	35	26	3	35
(2.7,2.9]	31	0	[36-380]	13	9	0	38	9	0	38
(2.9,3.2]	34	2	[10-162]	6	18	0	6	18	0	6
(3.2,3.7]	45	5	[7.1-380]	10	15	0	35	18	5	35
(3.7,4.1]	37	4	[0.4-370]	16	26	0	25	24	0	25
(4.1,4.6]	103	12	[3-340]	6	61	2	6	61	0	6
(4.6,5]	48	18	[0.3-162]	9	36	11	18	34	3	18
Total	545	63			354	19		364	15	

[a] Square brackets are inclusive: [0, 0.1] indicates locations with 0 ≤ RM ≤ 0.1. Left parenthesis indicates strictly greater than: (0.1, 0.3] captures locations with 0.1 < RM ≤ 0.3.

[b] Concentration ranges are provided for PCBs because the CV for PCBs was determined to be the most accurate and thus was used to develop the sampling design.

cPAH – carcinogenic polycyclic aromatic hydrocarbon
CV – coefficient of variation
dw – dry weight
MNR – monitored natural recovery
PCB – polychlorinated biphenyl
RI/FS – remedial investigation/feasibility study
RM – river mile
TEQ – toxic equivalent

The highly clustered nature of the historical sampling locations (Map B-1 and minimum distance noted in Table 1) made it inappropriate to calculate simple summaries of the mean and variance of the data within each segment. Instead, a simplified bootstrap estimate[9] of the coefficient of variation (CV) for each of the three COCs indicated that the site-wide CVs for total PCBs and cPAH TEQ were similar, while the CVs for arsenic were slightly lower (Table 2). Using the highest CVs to inform the study design provides appropriate estimates of the expected RME for the most variable analytes, and a buffer on the expected RME for analytes with lower CVs. Although the CVs for total PCBs and cPAH TEQ were similar, the CV for total PCBs was considered more accurate because many more total PCB than cPAH TEQ samples have been analyzed throughout the LDW (Table 1). Consequently, the remainder of the sediment discussion in this appendix presents results from only the total PCBs data; it is assumed that the study design based on PCB data will result in similar or better RME values for the other COCs.

Table 2. Distribution of the surface sediment CVs across bootstrap replicates

COC	Minimum	1st Quartile	Median	Mean	3rd Quartile	Maximum
Total PCBs	0.6	0.8	0.8	0.8	0.8	1.0
cPAH TEQ	0.7	0.8	0.8	0.8	0.9	1.0
Arsenic	0.3	0.5	0.5	0.5	0.6	0.7

Note: Each bootstrap replicate (B = 1,000) was comprised of 100 observations randomly selected from the RI surface sediment dataset (Map B-1), with the stipulation that all sampling locations were separated by at least 200 ft.

COC – contaminant of concern

cPAH – carcinogenic polycyclic aromatic hydrocarbon

CV – coefficient of variation

PCB – polychlorinated biphenyl

RI – remedial investigation

TEQ – toxic equivalent

2.2 FISH AND CRAB TISSUES

The 2007 RI fish and crab tissue data were used to assess variability among composites for the tissue types and species targeted in the baseline sampling (Table 3). Data from 2007 were primarily used because earlier data were temporarily elevated following dredging in both the LDW (e.g., Duwamish/Diagonal early action event) and East Waterway. Because of the paucity of information for Dungeness crab in the 2007 dataset, results from 2004 and 2005 (Windward 2010) were used to provide additional information regarding variance.

In 2007, composite samples were collected within four reaches, with RI reaches T1 and T2 contained within baseline Reach 1 (RM 0.0 to RM 2.9) and RI reaches T3 and T4 contained within baseline Reach 2 (RM 2.9 to RM 5.0). Samples from the different

[9] Each bootstrap replicate (B = 1,000) drew a random sample of 100 observations without replacement from the RI dataset, with the stipulation that sampling locations were separated by at least 200 ft.

reaches had different mean concentrations, so data from within the RI reaches were appropriately combined using a stratified model to estimate the variability of the site-wide mean for the proposed baseline survey (Table 3). When there are location effects within the population, a stratified model will produce a smaller standard error and hence, a smaller RME. The formulas used to calculate a stratified mean and standard deviation (SD) are provided in Section 5. Table 3 provides site-wide estimates of the mean and SD for each tissue type for both stratified models and single stratum models that would be appropriate if there were no differences in mean concentrations among the reaches.

The risk drivers for fish and crab tissues are PCBs and dioxins/furans. In this appendix, results for total PCBs (sum of Aroclors) are the only data evaluated for fish and crab tissues, because the dataset for total PCBs is more robust than the datasets for dioxins/furans.

Table 3. Summary statistics for the 2007 fish and crab tissue total PCB results, including the mean, SD, and CV

Baseline Reach	RI Reach	Tissue Type	N[a]	Mean Concentration (µg/kg, ww)	SD	CV	Comment
Dungeness crab							
1	T1	edible meat	1	15	na	na	4 individuals in this sample
	T1	whole body (calc'd)	1	97	na	na	4 individuals in this sample
	T2		0	na	na	na	no Dungeness caught in this reach
2	T3	edible meat	3	43	6.7	15%	
	T3	whole body (calc'd)	3	234	103	44%	footnote b
	T4		0	na	na	na	no Dungeness caught in this reach
Site wide – single stratum mean and SD		edible meat	4	36	15	42%	
		whole body (calc'd)	4	200	108	54%	
Site wide – stratified mean and SD		edible meat	4	36	6.7	19%	assumed SD from T3 for each reach
		whole body (calc'd)	4	200	103	52%	assumed SD from T3 for each reach[c]
English sole							
1	T1	fillet with skin	3	343	138	40%	
	T1	whole body	6	525	178	34%	
	T2	fillet with skin	3	293	107	36%	
	T2	whole body	6	693	219	32%	
2	T3	fillet with skin	3	403	78	19%	
	T3	whole body	6	893	364	41%	footnote b
	T4	fillet with skin	0	na	na	na	
	T4	whole body	1	300	na	na	
Site wide – single stratum mean and SD		fillet with skin	9	347	106	31%	
		whole body	19	683	300	44%	
Site wide – stratified mean and SD		fillet with skin	9	361	110	31%	used residual standard error as SD for each reach
		whole body	19	709	266	38%	used residual standard error as SD for each reach
Shiner surfperch							
1	T1	whole body	6	268	59	22%	
	T2	whole body	6	415	115	28%	

Baseline Reach	RI Reach	Tissue Type	N[a]	Mean Concentration (µg/kg, ww)	SD	CV	Comment
2	T3	whole body	6	763	314	41%	footnote b
	T4	whole body	4	315	66	21%	
Site wide – single stratum mean and SD		whole body	22	452	263	58%	
Site wide – stratified mean and SD		whole body	22	440	181	41%	used residual standard error as SD for each reach

[a] N = number of composite samples. The numbers of individuals per composite were: 5 individuals (Dungeness crab and English sole) and 10 individuals (shiner surfperch), unless otherwise noted.

[b] High variance was influenced by a single value. Without that value, the CV was greatly reduced, supporting increasing the number of fish per composite in baseline sampling, where feasible.

[c] High variance was influenced by a single hepatopancreas sample (individual values were 420, 520, and 1020 µg/kg ww). This elevated result is suspect, since this level of variability was not observed in the Dungeness crab composites from 2004 and 2005 datasets.

CV – coefficient of variation
PCB- polychlorinated biphenyl
SD – standard deviation
na – not applicable
RI – remedial investigation
ww – wet weight

3 Methods

3.1 SURFACE SEDIMENTS (0–10 CM)

The sampling programs represented in the RI/FS dataset used a variety of sampling designs with different objectives, and many of the sampling programs focused on smaller areas. As a result, the RI/FS dataset has irregular sampling densities across the site, including some areas with very tightly clustered samples and other areas with very few samples (Table 1, Map B-1). Using spatially clustered samples as if they were independent samples would likely result in biased estimates of mean and variance, which would not be representative of the expected site-wide conditions following active remediation.

Sampling variance is the variability of summary statistics (e.g., the mean) if the same sampling design, with the same sample size, were applied to the same population multiple times. A lower sampling variance results in improved precision in estimates of summary statistics. Some ways to reduce sampling variance include:

- Reducing variance among samples (e.g., by analyzing composites of multiple grab samples, thereby averaging over smaller scale variability)
- Increasing sample size throughout the site (e.g., a mean of 100 samples has lower variance than a mean of 20 samples)
- Using a stratified sampling design (e.g., by having higher sample densities within areas [strata] with higher variance or different means to reduce the sampling variability in the overall mean)

To use the existing data from MNR areas (Map B-1) to assess the benefits of different sampling approaches and determine which could be most efficiently used to improve precision, three key questions were asked. These questions, and the methods used to answer them, are described below.

3.1.1 Question 1

What minimum separation distance between samples would be required to produce spatially independent data?

The minimum separation distance between samples was required to reduce the bias and redundancy of information resulting from the tightly clustered samples within the RI dataset. The minimum separation distance was used to restrict how the data within the RI dataset were sampled in the bootstrapping exercise.

- **Method**: A correlogram displays the average spatial correlation (Moran's I) between pairs of samples within increasing distance intervals. The distance interval at which the correlation becomes nominal was used to determine the

minimum separation distance. Correlograms were created using *correlog{pgirmess}* (Giraudoux 2016) in R (R Core Team 2016).

3.1.2 Question 2

What is the variance of concentrations within different reaches of the LDW, and is it approximately consistent throughout the LDW?

If the spatial variance were very different within different sections of the river, this would indicate that variance strata exist and precision of the site-wide mean could be improved by stratifying the river and taking more samples where variance is higher.

- **Method:** Random groups of five adjacent samples were bootstrapped from the RI dataset. A sample size of five was chosen to mimic the sample sizes that will be used in composite sampling, and 5,000 bootstrap samples were drawn. Within each group, the randomly selected samples were separated by the minimum distance established by the answer to Question 1, and no more than a maximum distance of 1,320 ft (0.25 mi). This maximum separation distance was used because it was large enough to not limit the number of bootstrapped sample groups that could be formed, but not so large as to average over spatial patterns in concentrations that were present in this dataset. The variability within these groups of five samples was plotted against location along the river (average river mile of the five samples within the group). Any large changes in the magnitude of variance at different river miles would support the use of a stratified sampling design.

3.1.3 Question 3

What is the expected sampling variance for the LDW-wide mean using a set of 100 spatially balanced random samples combined into 20 composite samples?

- **Method**: Simulations of 20 independent composites, each containing 5 subsamples, were bootstrapped from the existing data to estimate variance in the mean of 20 composite samples. If the answer to Question No. 2 indicated that variance strata exist, sampling would be specified within these strata. Otherwise, sampling would occur throughout the river without specification of separate strata. The specific steps in the bootstrap approach for a non-stratified design are detailed below.

  1. Divide the 5 mi of the LDW into 20 segments of approximately equal area.[10]

[10] These segments were different than the conceptual composite areas proposed for the baseline sampling (Map 3-2 of the main document). The areas on Map 3-2 may not have had enough data points in this dataset to support the bootstrap subsampling (e.g., none of the EAAs were represented in this dataset). The segment boundaries used for this bootstrapping constrained the number of samples available for each random draw (Table 1). These boundaries were chosen to capture enough data points distributed throughout each segment to ensure that the full range of concentrations within the segment would be

2. Subsample within each segment to collect five samples separated by a minimum distance (i.e., the answer to Question 1).
    a. Record the mean for these five samples as the composite sample estimate; treatment of non-detects used substitution at one-half the detection limit (DL).[11]
    b. Record the SD for these five samples as the within-composite SD (note: this would not be observed in the baseline sampling, because all individual samples would not be analyzed, although they would be archived).
    c. Record the minimum, maximum, and average distances between samples to verify bootstrap methods.
3. Repeat Step 2 within each of the 20 segments.
4. Store the 20 simulated composites as a single bootstrap replicate of the LDW-wide sample.
    a. Record the mean, SD, skewness, and kurtosis for the bootstrap sample.
    b. Test the goodness-of-fit (GOF) of the bootstrap sample to a normal distribution (Shapiro-Wilk's test), and record the p-value. Non-rejection of the normality test justifies the use of the *t*-interval to estimate the 95UCL for the site-wide mean; otherwise, a 95UCL for a gamma-distributed dataset would be appropriate.
5. Repeat Steps 2 through 4 many times (B = 10,000) to develop a distribution of expected mean and sampling variance.

Section 4.1 presents the results from the analyses described above to answer the preceding questions. The outcome of the GOF test and estimate of the CV for each bootstrap replicate (Step 4) were used to estimate the RME for the mean from a sample design that utilized a spatially balanced collection of 20 composite samples (Section 6.1).

3.2 FISH AND CRAB TISSUES

In the baseline sampling to be conducted, English sole and Dungeness crab specimens will be collected and composited within each of two reaches of the LDW: Reach 1 (RM 0.0 to RM 2.9) and Reach 2 (RM 2.9 to RM 5.0) (Map 3-8 of the main document). Shiner surfperch specimens will be collected and composited within each of four subreaches, each comprising one-fourth of the LDW: subreach 1a (RM 0.0 to RM 1.25),

represented across the bootstrap replicates. Different segment boundaries could yield slightly different results for any one sample, but the distribution and density of data points in this dataset were large enough that large differences in the overall sampling variance are not expected.

[11] Preliminary simulations compared results between substitution using full and one-half DL to estimate the mean. Due to the high detection frequency, the method used to treat non-detects had very little effect on the outcome.

subreach 1b (RM 1.25 to RM 2.5), subreach 2a (RM 2.5 to RM 3.75), and subreach 2b (RM 3.75 to RM 5.0) (Map 3-9 of the main document). Four subreaches are being sampled for shiners instead of two because tissue data collected as part of the RI (Windward 2010) indicated that PCB concentrations and PCB congener patterns showed more spatial differentiation for shiner surfperch than for other fish and crab species analyzed in the RI.

In the 2007 RI/FS dataset, differences in mean concentrations were observed among the reaches (Table 3 and Figure 1). Consequently, a stratified model was the most appropriate model to estimate the site-wide mean and sampling variance for fish and crab tissues, with each reach or subreach having equal weight. A stratified model was applied to the data from the 2007 RI dataset, and means, SDs, and residuals from the stratified model were used to estimate site-wide CVs and examine distributional characteristics of the data (e.g., approximately normal or gamma distributed). Summary statistics (mean, SD, and CV) are summarized in Table 3 by reach, and site-wide estimates are presented for both a stratified model and using a pooled (single stratum) estimate.

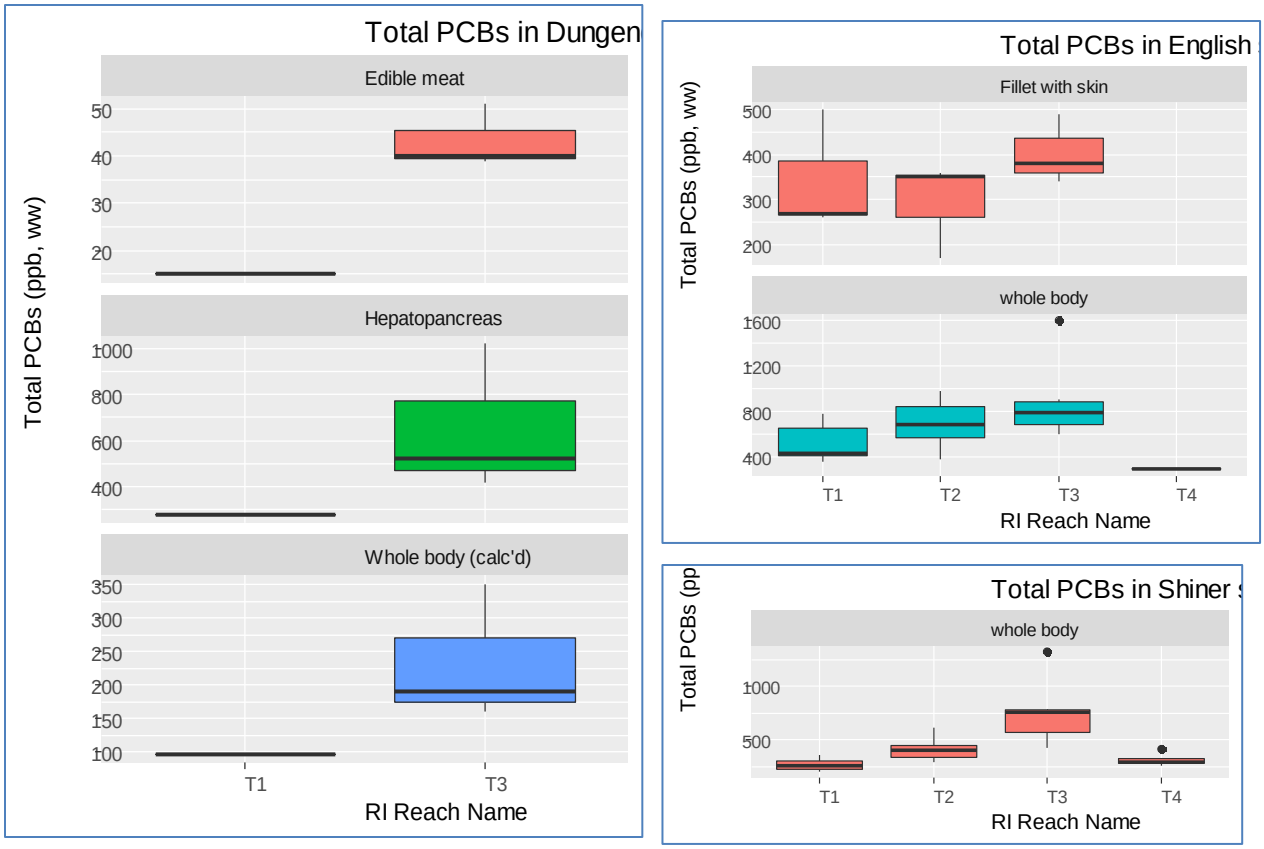


Figure summary statistics are presented in Table 3

Figure 1. Boxplots showing the distribution by reach of total PCBs (ppb, ww) within each species and tissue type for samples in the RI dataset

A GOF test (Shapiro-Wilk's test for normal distribution) and probability plots (QQ plots) were used to evaluate the distribution of each tissue type for each species. Due to the small sample sizes within each RI reach and evidence that a stratified model was appropriate for the site-wide mean (Table 3 and Figure 1), residuals from the stratified model (the differences between each observation and the reach mean) were combined across all RI reaches to evaluate the statistical distribution for each species and tissue type.

The GOF results are presented in Section 4.2. The best-fit distribution from the GOF evaluation and estimates of the CV for each tissue type and species were used to generate plots illustrating the expected RME of the mean as a function of sample size (Section 6.2).

4 Results

4.1 SURFACE SEDIMENTS (0–10 CM)

4.1.1 Question 1

The correlogram for total PCBs in sediments (Figure 2) suggests that the spatial correlation is strongest within approximately the first 200 ft. Beyond 300 ft, the correlation is low (in the range of 0.15) and appears to be within the noise of the random correlations present at further distances. Since it appears that samples within 200 ft are, in general, too highly correlated to be considered spatially independent, a minimum separation distance of 200 ft is used for the bootstrap sampling in the subsequent evaluations reported in this appendix.

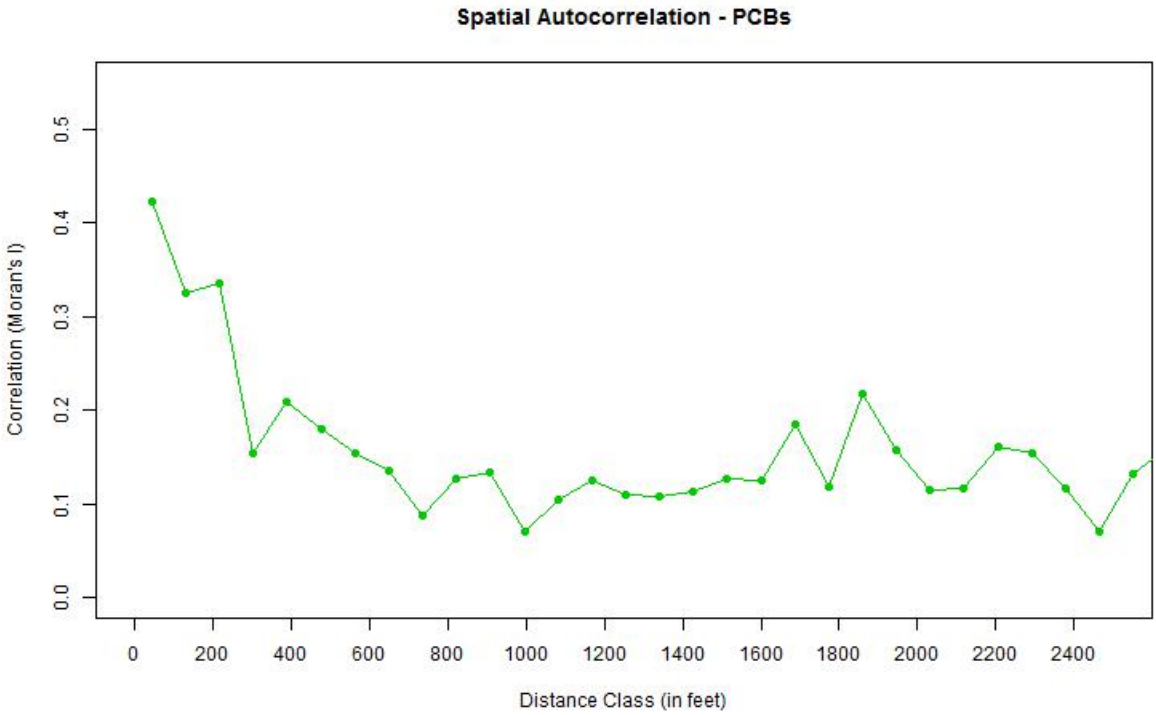


Figure 2. Correlogram (Moran's I versus distance) for total PCBs in the RI dataset

4.1.2 Question 2

The SDs within bootstrapped groups of five samples that were separated by distances between 200 and 1,320 ft (B = 5,000) were plotted against river mile (Figure 3). These results provided a measure of mid-range (200 ft to 0.25 mi)[12] spatial variability across the LDW. This investigation addressed the question of whether variance strata exist

[12] The approximate scale of separation present among individual samples contributing to a single composite sample in the proposed study design.

within the site. The magnitude of the SDs within sample groups of five was fairly consistent throughout the length of the river (Figure 3). A few exceptions included the areas below RM 0.5 and between RM 2.0 and RM 2.6. These areas with lower variance tended to have fewer samples, so it was assumed that the full variance in these areas was not sampled. These results indicate that dominant variance strata are absent and the entire river can be sampled with the same density throughout.

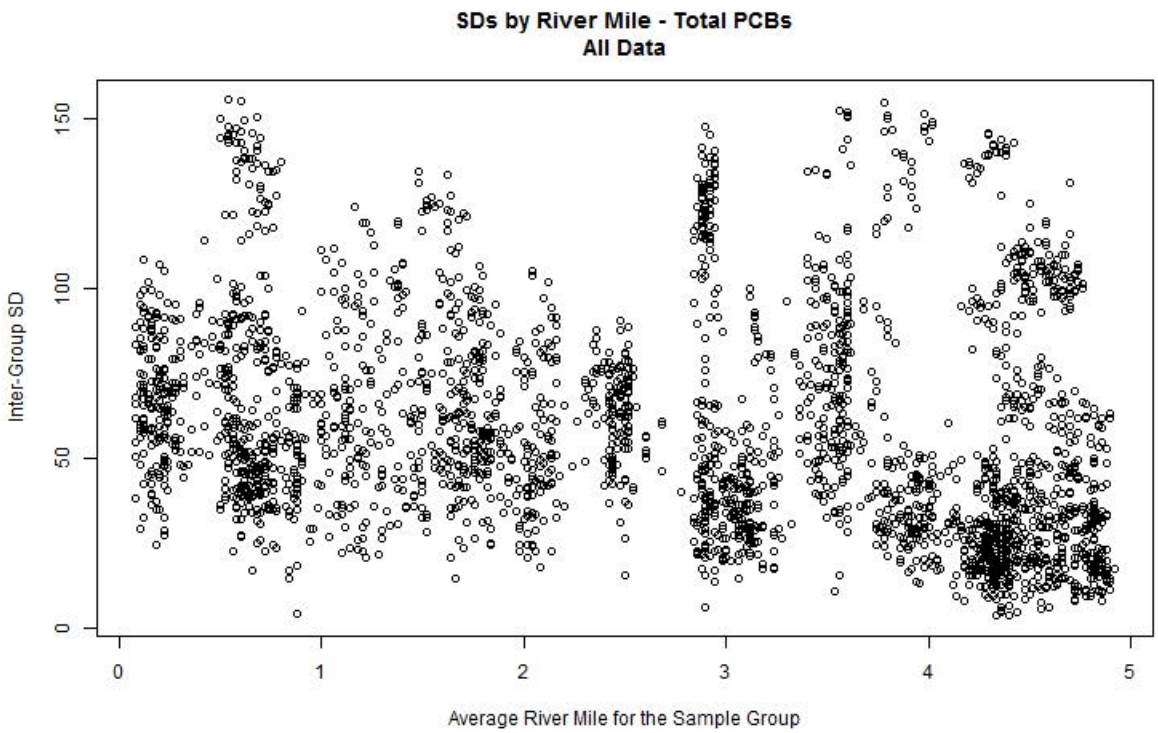
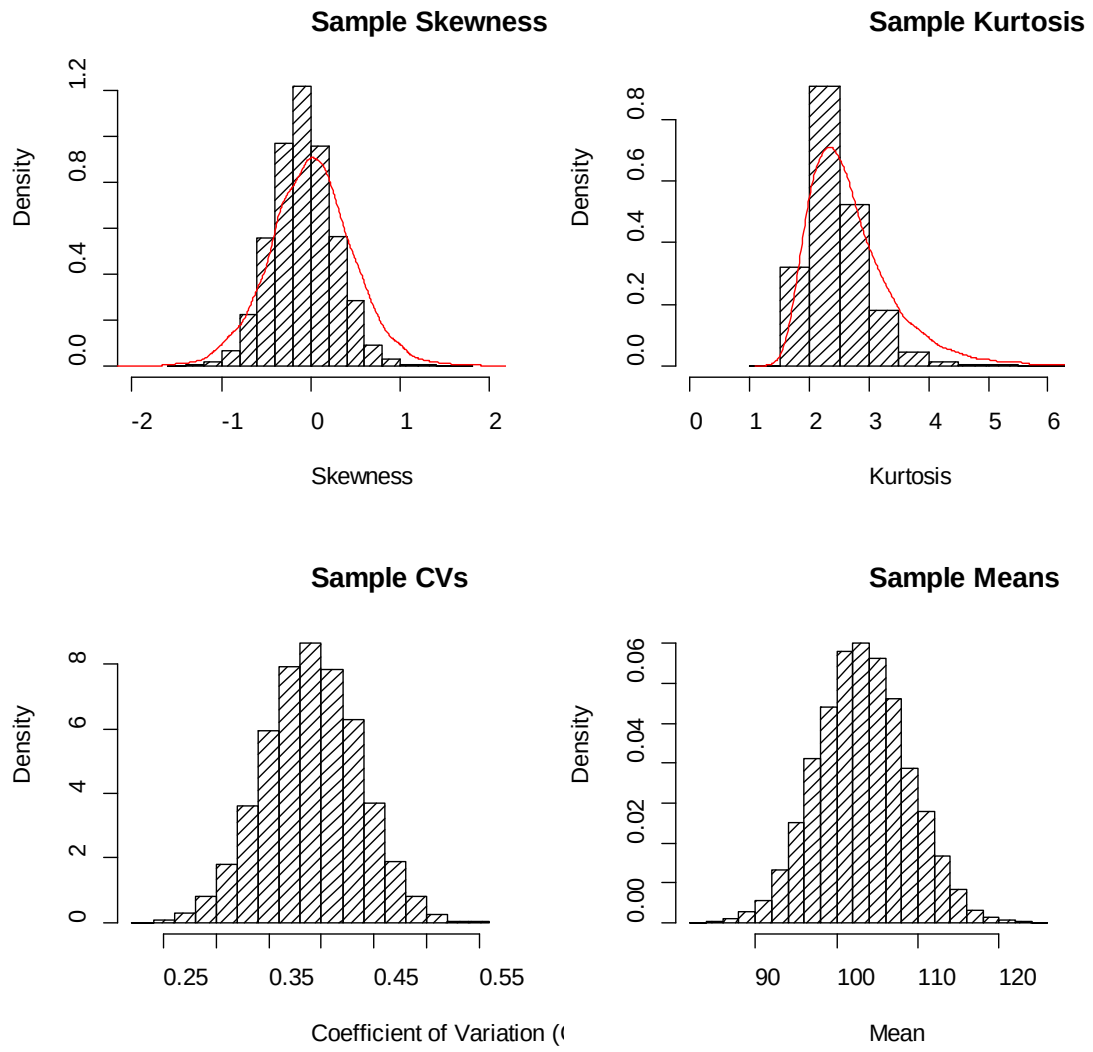


Figure 3. Inter-group SDs for bootstrap sample groups within 200 and 1,320 ft, plotted against the average river mile

4.1.3 Question 3

Because no strata were identified (via Question 2), LDW-wide bootstrap sampling was conducted as described in Section 3.1 using a non-stratified design. The frequency distributions of skewness and kurtosis for the bootstrapped samples indicated that these samples were similar to simulated normal samples of the same size (Figure 4). The bootstrapped samples were generally symmetric (skewness values near 0, Table 4) with a tendency for flatter distributions (kurtosis values less than 3) and a low probability of outliers (few kurtosis values greater than 4, Table 4). The sampling distribution of the mean (Figure 3) is strongly Gaussian, an expected result based on the Central Limit Theorem (CLT).[13]

[13] The CLT establishes that the mean of a sample randomly drawn (from any distribution) will approach normality as sample size increases.



Sample size of 20 within each bootstrap replicate, B = 10,000. The red line overlaid on the skewness and kurtosis histograms shows values for simulations of normally distributed samples of size 20.

Figure 4. Frequency distributions of summary statistics (skewness, kurtosis, coefficient of variation, and mean) from each LDW-wide bootstrap replicate

Table 4. Distribution of skewness, kurtosis, and CV for samples of size 20, across 10,000 bootstrap replicates

	Minimum	1st Quartile	Median	Mean	3rd Quartile	95th Percentile	Maximum
Skewness	-1.4	-0.3	-0.1	-0.1	0.1	0.5	1.7
Kurtosis	1.4	2.1	2.4	2.4	2.7	3.3	6.3
CV	0.23	0.36	0.39	0.39	0.42	0.46	0.55

CV – coefficient of variation

The distribution of the 20 composites within each bootstrap replicate was rejected as normally distributed (Shapiro-Wilks $p < 0.05$) in less than 2% of the bootstrap replicates. This is less than the 5% expected by chance, so these results support the expectation that a set of 20 spatially balanced composite samples from the post-remediated LDW will be a normally distributed sample.

The distribution of sample CVs had an average of 0.4, a 95th percentile of 0.46, and a maximum value of 0.55 across the 10,000 bootstrap replicates (Figure 3, Table 4). The average and maximum CVs from this distribution will be used in the sample size estimation presented in Section 6.

4.2 Fish and Crab Tissues

Composite tissue concentrations for each species and tissue type appeared to be approximately normally distributed, based on Shapiro-Wilk's GOF test (Table 5) and normal probability plots (Figure 5). Both of these evaluations used the residuals from a stratified model, after excluding two high values identified as outliers (one for English sole, whole body, and one for shiner surfperch, whole body). When the outliers were included, they dominated the probability plots and caused the normality assumption to be rejected. If the tissue data from the baseline sampling effort is skewed, a gamma distribution may be a more appropriate model. Consequently, sample size estimates for both normal and skewed gamma distributions are presented in Section 6.2.

Table 5. Results of the GOF tests on residuals pooled across RI reaches, reported by species and tissue type

Species	Tissue Type	N	Shapiro-Wilk's p-value	Comment
Dungeness crab	edible meat	4	0.31	insufficient data to assess distribution
	whole body (calc'd)	4	0.50	insufficient data to assess distribution
English sole	fillet with skin	9	0.53	data look normal
	whole body	18	0.63	normality rejected for all data; results shown excluding outlier at 1,600 ppb
Shiner surfperch	whole body	21	0.94	normality rejected for all data; results shown excluding outlier at 1,330 ppb

Note: Residuals are the differences between each composite value observation and the mean value of the RI reach.
GOF – goodness-of-fit
ppb – parts per billion
RI – remedial investigation

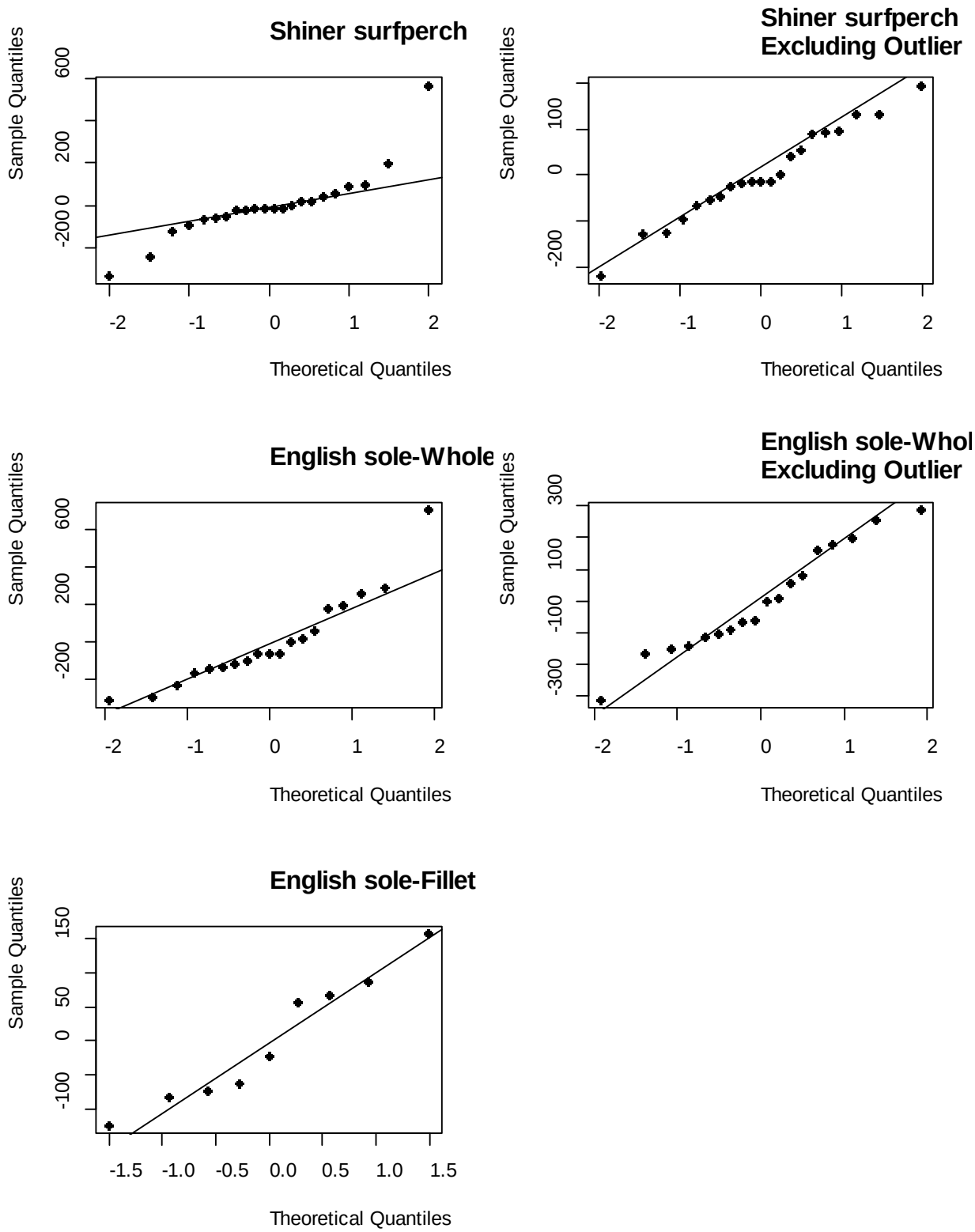


Figure 5. Normal probability plots of the concentration residuals within each RI reach, by species and tissue type for Shiner surfperch and English sole

The compositing methods used in the RI will be modified for the baseline sampling in order to meet the more general objectives of the baseline sampling, and also to reduce variance and the possibility for extreme values. Each composite sample will be comprised of individuals collected throughout the entire reach rather than within smaller subareas. The number of individuals per composite will be increased from 5 to 10 English sole and from 10 to 15 shiner surfperch. More individual crabs per composite sample will not be targeted because of the difficulty in catching the targeted size of Dungeness crab in the LDW.

The changes to the sampling approaches for English sole and shiner surfperch are expected to reduce variance and improve normality from what was observed in the 2007 dataset. The relationship between RME and sample size was calculated and presented for both a normal and a skewed (gamma) distribution (Section 6.2).

The targeted sample size can be identified for each species and tissue type using the curve associated with the appropriate CV value. The applicable CV values derived from the RI dataset were presented in Table 3 and are discussed in more detail below:

- **Dungeness crab – edible meat**: CV ≅ 20%. There were only three Dungeness crab edible meat composites in the 2007 dataset from which variance could be estimated. These three composites from RI reach T3 had a CV of 15%. Additional information from the 2004 dataset indicated that composite samples from reaches T1 and T3 (n = 3 each) both had CVs of 20%. In 2007, there appeared to be differences in concentrations among reaches, justifying the use of a stratified mean.
- **Dungeness crab – whole body (calculated[14])**: CV < 50%. There were only three Dungeness crab (calculated) whole-body composites in the 2007 dataset from which variance could be estimated. These three composites from RI reach T3 had a CV of 44%, an estimate that was heavily influenced by a single high hepatopancreas result.[15] Additional information from the 2004 and 2005 datasets suggests variability in the calculated whole-body crab values may be much lower than was observed in 2007. The site-wide CV of calculated whole-body values was 12% in 2004 (n = 7) and 4% in 2005 (n = 3). It appears that there may be much less variability among calculated whole-body crab estimates than suggested by the 2007 results alone, so a CV of 50% represents an extreme upper bound, and the actual value is expected to be much lower. Concentration differences were apparent among reaches, lending support to the use of a stratified mean.
- **English sole – fillet with skin**: CV ≅ 30%. Variance was based on three composites from each of three RI reaches (T1, T2, and T3). There did not appear to be strong differences in concentrations among reaches. Therefore, if the data

[14] Each whole-body crab composite concentration was calculated as the weighted sum of separate hepatopancreas and edible meat composites from the same crabs.

[15] The three hepatopancreas results were 420, 520, and 1020 µg/kg wet weight (ww).

support using a single population estimate (instead of a stratified estimated), this approach will gain one additional degree of freedom. Increasing the number of individuals per composite from 5 to 10 should reduce the variability in the baseline survey from what was observed in 2007.

- **English sole – whole body**: CV ≅ 40%. Variance was based on six composites from each of three RI reaches (T1, T2, and T3). Increasing the number of individuals per composite from 5 to 10 should reduce the variability in the baseline survey from what was observed in 2007.
- **Shiner surfperch – whole body**: CV ≅ 40%. Variance was based on six composites from each of three RI reaches (T1, T2, and T3) and four composites from RI reach T4. The mean concentrations within each RI reach were different, and the standard deviations increased with the means, supporting the use of a stratified mean. Increasing the number of individuals per composite from 10 to 15 and compositing throughout each reach should reduce the variability in the baseline survey from what was observed in 2007.

5 Formulas for the 95UCL for the Mean

5.1 Surface Sediments (0–10 cm)

Supported by the results in Section 4.1.3 and the CLT, the sampling distribution of the mean (n = 20 composite samples) is expected to be normally distributed. The *t*-interval can be used to calculate the 95UCL of the site-wide mean of a single population as:

$$\mathbf{95}\boldsymbol{UCL} = \bar{\boldsymbol{X}} + \boldsymbol{t}_{(\mathbf{0.05},\boldsymbol{n}-\mathbf{1})}\frac{\boldsymbol{SD}(\boldsymbol{X})}{\sqrt{\boldsymbol{n}}} \qquad \textbf{Equation 1}$$

Where:

$\bar{X}$ is the average of the *n* samples.

$SD(X)$ is the standard deviation of the *n* samples.

$t_{(0.05,n-1)}$ is the critical value from the t-distribution with 5% in the upper tail, and *n*-1 degrees of freedom.

5.2 Fish and Crab tissues

The fish and crab tissues will be collected and composited from individual subreaches (shiner surfperch) or reaches (English sole and crab). If it appears that the mean concentrations are different among reaches, stratified estimators will be used to reduce the variance of the site-wide mean.

Using equal weights for each reach, the site-wide mean can be estimated as the grand mean of the mean concentrations within each reach as follows:

$$\bar{\bar{X}} = w \sum_{i=1}^{k} \bar{X}_i \qquad \textbf{Equation 2}$$

Where

$\bar{X}_i$ is the average concentration in reach i (i = 1 to k, where k = 2 for English sole and Dungeness crab; and k= 4 for Shiner surfperch).

$w = 1/k$ (i.e., ½ for sole and crab, and ¼ for perch).

The sampling variance of the stratified mean is:

$$\widehat{Var}(\bar{\bar{X}}) = w^2 \sum_{i=1}^{k} S_{\bar{X}_i}^2 \qquad \textbf{Equation 3}$$

Equation 3 simplifies to the following when each of the *k* reaches are weighted equally:

$$\widehat{Var}(\bar{\bar{X}}) = \frac{1}{k^2} \sum_{i=1}^{k} s_{\bar{X}_i}^2 \qquad \textbf{Equation 4}$$

Where

$s_{\bar{X}_i}^2 = {s_i^2}/{n_i}$

s_i^2 is the usual sample variance estimate of the n_i observations in reach i (i = 1 to k, k = 2 for sole and crab, and k = 4 for perch).

n_i is the sample size in reach i.

For a stratified mean, the CLT is invoked for the UCL estimate (Levy and Lemeshow 1999), although a more conservative Student's *t*-interval is used instead of a Z-interval due to the uncertainty inherent in small samples with an unknown population variance.

$$95UCL = \bar{\bar{X}} + t_{(0.05,df)} \times SE(\bar{\bar{X}}) \qquad \textbf{Equation 5}$$

Where:

$\bar{\bar{X}}$ is the site-wide mean, as calculated above.

SE($\bar{\bar{X}}$) is the standard error of the stratified mean, equal to the square root of the variance estimator in Equation 4.

df = the degrees of freedom for this estimator would normally be estimated using Satterthwaite's formula which is a function of variance. For the purposes of this *a priori* sample size estimation, the degrees of freedom will be set to $N - k$ (N = the total number of samples site-wide, k = the number of strata).

If the population does not appear to have different means or variances within the different reaches, then the results from all reaches will be pooled for greater power. These pooled data may either be approximately normally distributed (Equation 1), or gamma distributed, which uses the following equations.

$$\boldsymbol{Approximate\ 95UCL = 2n\hat{k}\bar{X}/\chi^2_{(0.05,df=2n\hat{k})}} \qquad \textbf{Equation 6}$$

Where:

$\hat{k}$ is the shape estimator for the gamma distribution.

$\bar{X}$ is the mean.

$\chi^2_{(0.05,df=2n\hat{k})}$ is the 5th quantile of the chi-square distribution (i.e., 5% of the area is in the left tail), with $2n\hat{k}$ degrees of freedom.

For a gamma distribution, the mean and SD are functions of the scale and shape parameters, Θ and k, as: $\bar{X} = \Theta k$ and $SD = \Theta\sqrt{k}$. Thus, the CV = $\Theta\sqrt{k}/\Theta k = 1/\sqrt{k}$ and $k = 1/CV^2$, and Equation 7 expressed in terms of the CV reduces to the following (EPA 2013):

$$\boldsymbol{Approximate\ 95UCL = \frac{2n}{CV^2}\bar{X}/\chi^2_{(0.05,df=2n/CV^2)}} \qquad \textbf{Equation 7}$$

And the RME as a proportion of the mean is:

$$\boldsymbol{RME = \frac{\left(\frac{2n}{CV^2}\bar{X}/\chi^2_{(0.05,df=2n/CV^2)} - \bar{X}\right)}{\bar{X}} = \frac{2n}{CV^2}/\chi^2_{(0.05,df=2n/CV^2)} - 1} \qquad \textbf{Equation 8}$$

5.3 Intertidal Sediments (0–45 cm) for Direct Contact During Beach Play

Three composite samples will be available from each beach to estimate the 95UCL for each. The shape of the distribution cannot be properly evaluated with only three samples, so the central limit theorem is invoked and normality is assumed. Based on this assumption, the 95UCL will be derived for each beach using the standard equation for a normally distributed population (Equation 1) with n = 3, and $\bar{X}$ and SD(X) the mean and standard deviation, respectively, of the three samples from each beach.

5.4 Intertidal Sediments (0–45 cm) for Direct Contact During Clamming

Three composites samples, each representing the site-wide average, will be used to estimate the 95UCl of the site-wide mean. The shape of the distribution cannot be

properly evaluated with only three samples, so the central limit theorem is invoked and normality is assumed. Based on this assumption, the 95UCL will be derived with the standard equation for a normally distributed population (Equation 1) with n = 3, and $\bar{X}$ and SD(X) the mean and standard deviation, respectively, of the three samples across the site.

5.5 CLAM TISSUES

Eleven composite tissue samples will be collected during baseline sample, each representative of a single local clam tissue collection area. The 11 samples will be used to calculate the site-wide 95UCL for comparison to target tissue levels. This assumes each clam collection area is equally likely to be visited by any person at any point in time over the 30- (non-tribal) and 70-year (adult tribal) exposure periods. Once these data are available, the distribution will be assessed using GOF tests and probability plots. The most appropriate methods will be used to calculate the 95UCL

6 Discussion and Conclusions

The sampling designs for both surface sediment (0–10 cm) and fish and crab tissues are intended to meet the RME target of 25% for the site-wide means.

6.1 SURFACE SEDIMENTS (0–10 CM)

The distribution of the mean of 100 samples drawn from the same population is expected to be approximately normal based on the CLT and the law of large numbers. When the 100 samples are combined into 20 averages (composites), the distribution of the mean is still expected to approach normality through the CLT. The bootstrap estimates from existing data that were used to simulate the post-remediated LDW concentration distributions illustrated that the sampling distribution of the mean was indeed Gaussian (Figure 3). In addition, the 20 composite samples were consistently normally distributed (Section 4.1.3). These results support the use of a normal t-interval to calculate the 95UCL for the site-wide mean (Equation 1).

Using Equation 1 for the 95UCL and n = 20, the RME is calculated as

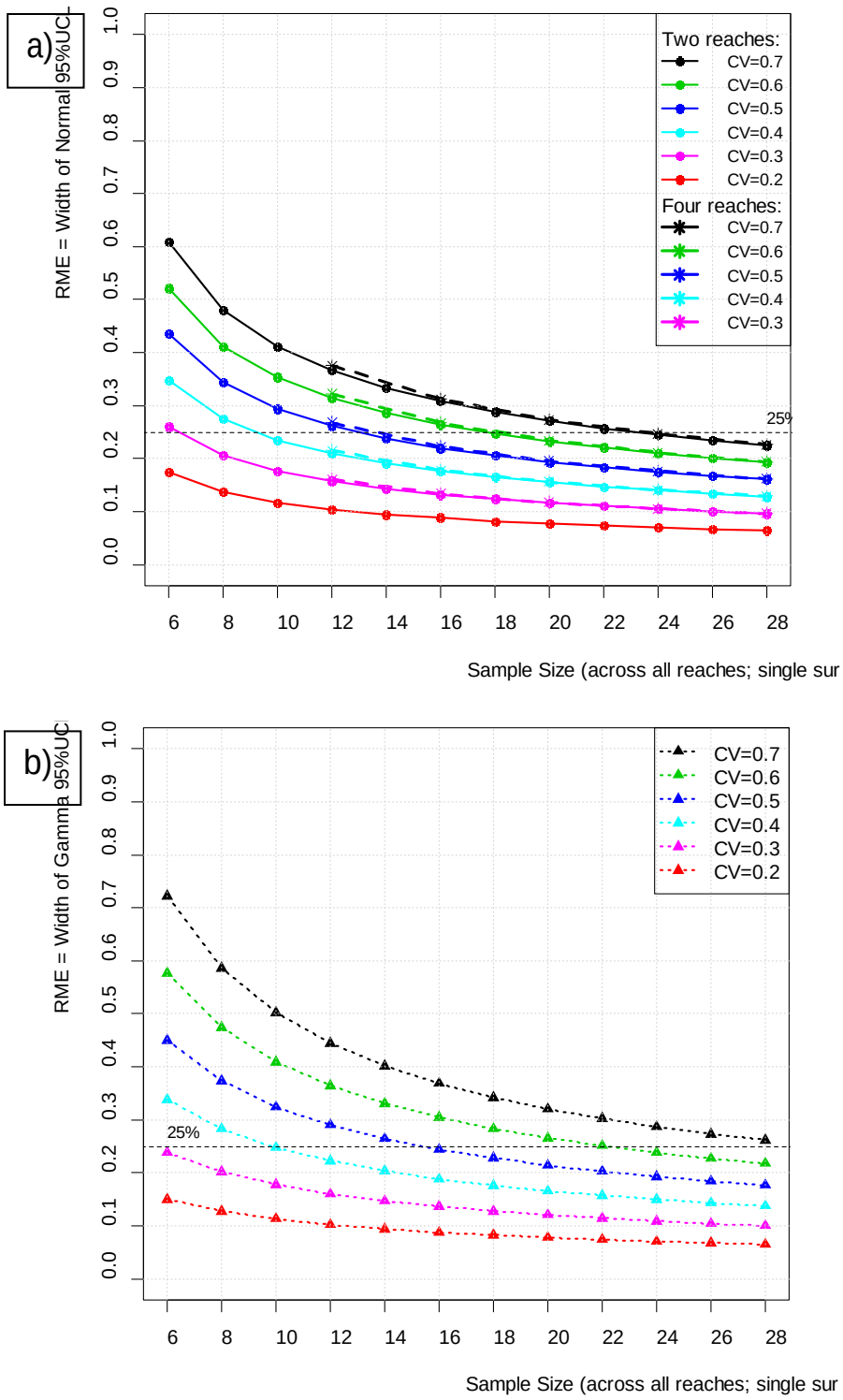
$$\boldsymbol{CV} \times \frac{\boldsymbol{t}_{(0.05,20-1)}}{\sqrt{\mathbf{20}}} \times \mathbf{100.}$$

For CVs ranging from 0.4 to 0.6 (the median to a value exceeding the maximum CV observed in the bootstrap results), the proposed sampling design of 20 composite samples (100 spatially balanced samples, combined into 20 composites of 5 samples each) is expected to achieve an RME for the post-remediated site-wide mean of approximately 15 to 23%.

6.2 FISH AND CRAB TISSUES

The distribution of the fish and crab tissue composites was observed to have outliers in some of the tissue types (Section 4.2). The increase in the number of fish per composite and inclusion of fish across a larger area for each composite is expected to reduce the chance of outliers justifying the use of Student's t-interval for the 95UCL (Equation 5). If the baseline data are skewed, the use of a gamma distribution 95UCL will be more appropriate (Equation 7). The CVs assumed to be most applicable for these data (Section 4.2) include the observed extreme values, with the exception of the Dungeness crab (calculated) whole-body estimate.

Figure 6 illustrates the relationship between the total number of composite samples and the RME, for normal, stratified estimators of the mean (Figure 6a) and for a single gamma-distributed population (Figure 6b), for a range of CVs. Results are displayed for two strata (applicable to English sole and Dungeness crab) and four strata (applicable to shiner surfperch).



Shown for a range of CVs for samples balanced across two or four reaches.

Figure 6. RME for two or four strata, using a normal UCL (top) and for a single population using a gamma UCL (bottom) versus total sample size

A site-wide total of 12 composite samples of each tissue type for English sole (6 in each of 2 reaches) and shiner surfperch (3 in each of 4 subreaches) is expected to meet the target RME of 25% or better for these species and tissue types, based on CVs of 0.4 or less. The CVs observed in the 2007 dataset were 0.3 to 0.4 for these tissue types, and baseline sampling is expected to be less variable because more individuals will be included in each of the composite samples.

A site-wide total of 12 composite samples for Dungeness crab edible meat (6 in each of 2 reaches) is expected to meet a target RME of approximately 10%, based on a CV of 0.2. The whole-body (calculated) results had high variability in the 2007 dataset, but this was influenced by a single high hepatopancreas sample. Information from the 2004 and 2005 datasets suggests that the CV may be much lower (≤ 0.12).

6 References

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APPENDIX B. ANALYTICAL METHODS AND REPORTING LIMITS

Tables

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This appendix contains a subset of the tables with reporting limit goals and methods. The remaining tables of this type are included in the main text of the work plan. Tables were included in this appendix if they were for conventional parameters, components of sums, or of great length.

Table 1. Methods and RLs for conventional analyses

Analyte	Matrix	Method	Unit	RL
TOC	sediment	PSEP 1986 Combustion IR	% dw	0.0200
Total solids	sediment	SM 2540 G-97	% dw	0.04000
Grain size	sediment	PSEP 1986	% dw	0.1
Lipids	tissue	PSEP 1986	% ww	0.010
TSS	surface water	SM 2540 D-97	mg/L	1.0
TOC	surface water	SM 5310 B-00	mg/L	0.500
DOC	surface water	SM 5310 B-00	mg/L	0.500

DOC – dissolved organic carbon
PSEP – Puget Sound Estuary Program
RL – reporting limit
TOC – total organic carbon
TSS – total suspended solids

Table 2. Methods and RL goals for tissue analytes that are components of sums

Analyte	Method	Unit	RL
cPAHs			
Benzo(a)anthracene	EPA 8270D-SIM	µg/kg ww	5.00
Benzo(a)pyrene	EPA 8270D-SIM	µg/kg ww	5.00
Total benzofluoranthenes	EPA 8270D-SIM	µg/kg ww	10.0
Chrysene	EPA 8270D-SIM	µg/kg ww	5.00
Dibenzo(a,h)anthracene	EPA 8270D-SIM	µg/kg ww	5.00
Indeno(1,2,3-cd)pyrene	EPA 8270D-SIM	µg/kg ww	5.00
Chlordanes			
alpha-Chlordane	EPA 8270D/1699 Mod	µg/kg ww	1.0
cis-Nonachlor	EPA 8270D/1699 Mod	µg/kg ww	1.0
gamma-Chlordane	EPA 8270D/1699 Mod	µg/kg ww	1.0
Oxychlordane	EPA 8270D/1699 Mod	µg/kg ww	2.5
trans-Nonachlor	EPA 8270D/1699 Mod	µg/kg ww	1.0
DDx Compounds			
2,4'-DDD	EPA 8270D/1699 Mod	µg/kg ww	2.5
2,4'-DDE	EPA 8270D/1699 Mod	µg/kg ww	2.5
2,4'-DDT	EPA 8270D/1699 Mod	µg/kg ww	1.0
4,4'-DDD	EPA 8270D/1699 Mod	µg/kg ww	1.0
4,4'-DDE	EPA 8270D/1699 Mod	µg/kg ww	2.5
4,4'-DDT	EPA 8270D/1699 Mod	µg/kg ww	1.0

cPAH – carcinogenic polycyclic aromatic hydrocarbon
DDD – dichlorodiphenyldichloroethane
DDE – dichlorodiphenyldichloroethylene
DDT – dichlorodiphenyltrichloroethane
EPA – US Environmental Protection Agency
RL – reporting limit
SIM – selective ion monitoring
DDx – DDT isomers (2,4′-DDD, 4,4′-DDD, 2,4′-DDE, 4,4′-DDE, 2,4′-DDT and 4,4′-DDT)

Table 3. Methods and RL goals for water analytes that are components of sums

Analyte	Method	Units	RL
Chlordanes			
alpha-Chlordane	EPA 8081B	µg/L	0.025
cis-Nonachlor	EPA 8081B	µg/L	0.050
gamma-Chlordane	EPA 8081B	µg/L	0.025
Oxychlordane	EPA 8081B	µg/L	0.050
trans-Nonachlor	EPA 8081B	µg/L	0.050

EPA – US Environmental Protection Agency
RL – reporting limit

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-1	1.0	20.0	0.1	2.0	0.1	2.0
PCB-2	1.0	20.0	0.1	2.0	0.1	2.0
PCB-3	1.0	20.0	0.1	2.0	0.1	2.0
PCB-4	2.0	20.0	0.2	2.0	0.2	2.0
PCB-5	2.0	20.0	0.2	2.0	0.2	2.0
PCB-6	2.0	20.0	0.2	2.0	0.2	2.0
PCB-7	2.0	20.0	0.2	2.0	0.2	2.0
PCB-8	2.0	20.0	0.2	2.0	0.2	2.0
PCB-9	2.0	20.0	0.2	2.0	0.2	2.0
PCB-10	2.0	20.0	0.2	2.0	0.2	2.0
PCB-11	2.0	20.0	0.2	2.0	0.2	2.0
PCB-12/13	2.0	20.0	0.2	2.0	0.2	2.0
PCB-14	2.0	20.0	0.2	2.0	0.2	2.0
PCB-15	2.0	20.0	0.2	2.0	0.2	2.0
PCB-16	1.0	20.0	0.1	2.0	0.1	2.0
PCB-17	1.0	20.0	0.1	2.0	0.1	2.0
PCB-19	1.0	20.0	0.1	2.0	0.1	2.0
PCB-21/33	1.0	20.0	0.1	2.0	0.1	2.0
PCB-22	1.0	20.0	0.1	2.0	0.1	2.0
PCB-23	1.0	20.0	0.1	2.0	0.1	2.0
PCB-24	1.0	20.0	0.1	2.0	0.1	2.0

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-25	1.0	20.0	0.1	2.0	0.1	2.0
PCB-26/29	1.0	20.0	0.1	2.0	0.1	2.0
PCB-27	1.0	20.0	0.1	2.0	0.1	2.0
PCB-28/20	1.0	20.0	0.1	2.0	0.1	2.0
PCB-30/18	1.0	20.0	0.1	2.0	0.1	2.0
PCB-31	1.0	20.0	0.1	2.0	0.1	2.0
PCB-32	1.0	20.0	0.1	2.0	0.1	2.0
PCB-34	1.0	20.0	0.1	2.0	0.1	2.0
PCB-35	1.0	20.0	0.1	2.0	0.1	2.0
PCB-36	1.0	20.0	0.1	2.0	0.1	2.0
PCB-37	1.0	20.0	0.1	2.0	0.1	2.0
PCB-38	1.0	20.0	0.1	2.0	0.1	2.0
PCB-39	1.0	20.0	0.1	2.0	0.1	2.0
PCB-41/40/71	1.0	20.0	0.1	2.0	0.1	2.0
PCB-42	1.0	20.0	0.1	2.0	0.1	2.0
PCB-43	1.0	20.0	0.1	2.0	0.1	2.0
PCB-44/47/65	1.0	20.0	0.1	2.0	0.1	2.0
PCB-45/51	1.0	20.0	0.1	2.0	0.1	2.0
PCB-46	1.0	20.0	0.1	2.0	0.1	2.0
PCB-48	1.0	20.0	0.1	2.0	0.1	2.0
PCB-50/53	1.0	20.0	0.1	2.0	0.1	2.0
PCB-52	1.0	20.0	0.1	2.0	0.1	2.0
PCB-54	1.0	20.0	0.1	2.0	0.1	2.0
PCB-55	1.0	20.0	0.1	2.0	0.1	2.0
PCB-56	1.0	20.0	0.1	2.0	0.1	2.0
PCB-57	1.0	20.0	0.1	2.0	0.1	2.0
PCB-58	1.0	20.0	0.1	2.0	0.1	2.0
PCB-59/62/75	1.0	20.0	0.1	2.0	0.1	2.0
PCB-60	1.0	20.0	0.1	2.0	0.1	2.0
PCB-61/70/74/76	1.0	20.0	0.1	2.0	0.1	2.0
PCB-63	1.0	20.0	0.1	2.0	0.1	2.0
PCB-64	1.0	20.0	0.1	2.0	0.1	2.0
PCB-66	1.0	20.0	0.1	2.0	0.1	2.0

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-67	1.0	20.0	0.1	2.0	0.1	2.0
PCB-68	1.0	20.0	0.1	2.0	0.1	2.0
PCB-69/49	1.0	20.0	0.1	2.0	0.1	2.0
PCB-72	1.0	20.0	0.1	2.0	0.1	2.0
PCB-73	1.0	20.0	0.1	2.0	0.1	2.0
PCB-77	1.0	20.0	0.1	2.0	0.1	2.0
PCB-78	1.0	20.0	0.1	2.0	0.1	2.0
PCB-79	1.0	20.0	0.1	2.0	0.1	2.0
PCB-80	1.0	20.0	0.1	2.0	0.1	2.0
PCB-81	1.0	20.0	0.1	2.0	0.1	2.0
PCB-82	1.0	20.0	0.1	2.0	0.1	2.0
PCB-83/99	1.0	20.0	0.1	2.0	0.1	2.0
PCB-84	1.0	20.0	0.1	2.0	0.1	2.0
PCB-88/91	1.0	20.0	0.1	2.0	0.1	2.0
PCB-89	1.0	20.0	0.1	2.0	0.1	2.0
PCB-92	1.0	20.0	0.1	2.0	0.1	2.0
PCB-94	1.0	20.0	0.1	2.0	0.1	2.0
PCB-95/100/93/102/98	1.0	20.0	0.1	2.0	0.1	2.0
PCB-96	1.0	20.0	0.1	2.0	0.1	2.0
PCB-103	1.0	20.0	0.1	2.0	0.1	2.0
PCB-104	1.0	20.0	0.1	2.0	0.1	2.0
PCB-105	1.0	20.0	0.1	2.0	0.1	2.0
PCB-106	1.0	20.0	0.1	2.0	0.1	2.0
PCB-108/124	1.0	20.0	0.1	2.0	0.1	2.0
PCB-109/119/86/97/125/87	1.0	20.0	0.1	2.0	0.1	2.0
PCB-107	1.0	20.0	0.1	2.0	0.1	2.0
PCB-110/115	1.0	20.0	0.1	2.0	0.1	2.0
PCB-111	1.0	20.0	0.1	2.0	0.1	2.0
PCB-112	1.0	20.0	0.1	2.0	0.1	2.0
PCB-113/90/101	1.0	20.0	0.1	2.0	0.1	2.0
PCB-114	1.0	20.0	0.1	2.0	0.1	2.0
PCB-117/116/85	1.0	20.0	0.1	2.0	0.1	2.0

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-118	1.0	20.0	0.1	2.0	0.1	2.0
PCB-120	1.0	20.0	0.1	2.0	0.1	2.0
PCB-121	1.0	20.0	0.1	2.0	0.1	2.0
PCB-122	1.0	20.0	0.1	2.0	0.1	2.0
PCB-123	1.0	20.0	0.1	2.0	0.1	2.0
PCB-126	1.0	20.0	0.1	2.0	0.1	2.0
PCB-127	1.0	20.0	0.1	2.0	0.1	2.0
PCB-128/166	1.0	20.0	0.1	2.0	0.1	2.0
PCB-130	1.0	20.0	0.1	2.0	0.1	2.0
PCB-131	1.0	20.0	0.1	2.0	0.1	2.0
PCB-132	1.0	20.0	0.1	2.0	0.1	2.0
PCB-133	1.0	20.0	0.1	2.0	0.1	2.0
PCB-134/143	1.0	20.0	0.1	2.0	0.1	2.0
PCB-136	1.0	20.0	0.1	2.0	0.1	2.0
PCB-137	1.0	20.0	0.1	2.0	0.1	2.0
PCB-138/163/129/160	1.0	20.0	0.1	2.0	0.1	2.0
PCB-139/140	1.0	20.0	0.1	2.0	0.1	2.0
PCB-141	1.0	20.0	0.1	2.0	0.1	2.0
PCB-142	1.0	20.0	0.1	2.0	0.1	2.0
PCB-144	1.0	20.0	0.1	2.0	0.1	2.0
PCB-145	1.0	20.0	0.1	2.0	0.1	2.0
PCB-146	1.0	20.0	0.1	2.0	0.1	2.0
PCB-147/149	1.0	20.0	0.1	2.0	0.1	2.0
PCB-148	1.0	20.0	0.1	2.0	0.1	2.0
PCB-150	1.0	20.0	0.1	2.0	0.1	2.0
PCB-151/135/154	1.0	20.0	0.1	2.0	0.1	2.0
PCB-152	1.0	20.0	0.1	2.0	0.1	2.0
PCB-153/168	1.0	20.0	0.1	2.0	0.1	2.0
PCB-155	1.0	20.0	0.1	2.0	0.1	2.0
PCB-156/157	1.0	40.0	0.1	4.0	0.1	4.0
PCB-158	1.0	20.0	0.1	2.0	0.1	2.0
PCB-159	1.0	20.0	0.1	2.0	0.1	2.0
PCB-161	1.0	20.0	0.1	2.0	0.1	2.0

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-162	1.0	20.0	0.1	2.0	0.1	2.0
PCB-164	1.0	20.0	0.1	2.0	0.1	2.0
PCB-165	1.0	20.0	0.1	2.0	0.1	2.0
PCB-167	1.0	20.0	0.1	2.0	0.1	2.0
PCB-169	1.0	20.0	0.1	2.0	0.1	2.0
PCB-170	1.0	20.0	0.1	2.0	0.1	2.0
PCB-171/173	1.0	20.0	0.1	2.0	0.1	2.0
PCB-172	1.0	20.0	0.1	2.0	0.1	2.0
PCB-174	1.0	20.0	0.1	2.0	0.1	2.0
PCB-175	1.0	20.0	0.1	2.0	0.1	2.0
PCB-176	1.0	20.0	0.1	2.0	0.1	2.0
PCB-177	1.0	20.0	0.1	2.0	0.1	2.0
PCB-178	1.0	20.0	0.1	2.0	0.1	2.0
PCB-179	1.0	20.0	0.1	2.0	0.1	2.0
PCB-180/193	1.0	20.0	0.1	2.0	0.1	2.0
PCB-181	1.0	20.0	0.1	2.0	0.1	2.0
PCB-182	1.0	20.0	0.1	2.0	0.1	2.0
PCB-183/185	1.0	20.0	0.1	2.0	0.1	2.0
PCB-184	1.0	20.0	0.1	2.0	0.1	2.0
PCB-186	1.0	20.0	0.1	2.0	0.1	2.0
PCB-187	1.0	20.0	0.1	2.0	0.1	2.0
PCB-188	1.0	20.0	0.1	2.0	0.1	2.0
PCB-189	1.0	20.0	0.1	2.0	0.1	2.0
PCB-190	1.0	20.0	0.1	2.0	0.1	2.0
PCB-191	1.0	20.0	0.1	2.0	0.1	2.0
PCB-192	1.0	20.0	0.1	2.0	0.1	2.0
PCB-194	1.0	20.0	0.1	2.0	0.1	2.0
PCB-195	1.0	20.0	0.1	2.0	0.1	2.0
PCB-196	1.0	20.0	0.1	2.0	0.1	2.0
PCB-197/200	1.0	20.0	0.1	2.0	0.1	2.0
PCB-198/199	1.0	20.0	0.1	2.0	0.1	2.0
PCB-201	1.0	20.0	0.1	2.0	0.1	2.0
PCB-202	1.0	20.0	0.1	2.0	0.1	2.0

Table 4. RL goals for PCB congeners

Analyte	EPA Method 1668C					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
PCB-203	1.0	20.0	0.1	2.0	0.1	2.0
PCB-204	1.0	20.0	0.1	2.0	0.1	2.0
PCB-205	1.0	20.0	0.1	2.0	0.1	2.0
PCB-206	1.0	20.0	0.1	2.0	0.1	2.0
PCB-207	1.0	20.0	0.1	2.0	0.1	2.0
PCB-208	1.0	20.0	0.1	2.0	0.1	2.0
PCB-209	1.0	20.0	0.1	2.0	0.1	2.0

[a] EMDL is a sample-specific DL. The value provided here is an estimate, and the sample-specific values will vary based on sample mass and the analytical conditions at the time of analysis

[b] LMCL is Axys Analytical's lowest calibration limit. Detected values below the LMCL are J-qualified. The reported LMCL will be adjusted based on the sample mass of each sample.

DL – detection limit
EPA – US Environmental Protection Agency
EMDL – estimated method detection limit
LMCL – lower method calibration limit
PCB – polychlorinated biphenyl
RL – reporting limit

Table 5. RL goals for dioxins/furan congeners

Analyte	EPA Method 1613B					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
2,3,7,8-TCDD	0.50	2.0	0.05	0.2	0.05	0.20
1,2,3,7,8-PeCDD	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,4,7,8-HxCDD	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,6,7,8-HxCDD	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,7,8,9-HxCDD	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,4,6,7,8-HpCDD	0.50	10.0	0.05	1.0	0.05	1.00
OCDD	0.50	20.0	0.05	2.0	0.05	2.00
2,3,7,8-TCDF	0.50	2.0	0.05	0.2	0.05	0.20
1,2,3,7,8-PeCDF	0.50	10.0	0.05	1.0	0.05	1.00
2,3,4,7,8-PeCDF	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,4,7,8-HxCDF	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,6,7,8-HxCDF	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,7,8,9-HxCDF	0.50	10.0	0.05	1.0	0.05	1.00
2,3,4,6,7,8-HxCDF	0.50	10.0	0.05	1.0	0.05	1.00

Table 5. RL goals for dioxins/furan congeners

Analyte	EPA Method 1613B					
	Water (pg/L) based on a 1L sample		Sediment (ng/kg dw) based on 10g sample		Tissue (ng/kg ww) based on 10g sample	
	EMDL[a]	LMCL[b]	EMDL	LMCL	EMDL	LMCL
1,2,3,4,6,7,8-HpCDF	0.50	10.0	0.05	1.0	0.05	1.00
1,2,3,4,7,8,9-HpCDF	0.50	10.0	0.05	1.0	0.05	1.00
OCDF	0.50	20.0	0.05	2.0	0.05	2.00

[a] EMDL is a sample-specific DL. The value provided here is an estimate, and the sample-specific values will vary based on sample mass and the analytical conditions at the time of analysis

[b] LMCL is Axys Analytical's lowest calibration limit. Detected values below the LMCL are J-qualified. The reported LMCL will be adjusted based on the sample mass of each sample.

DL – detection limit
EPA – US Environmental Protection Agency
EMDL – estimated method detection limit
HpCDD – heptachlorodibenzo-p-dioxin
HpCDF – heptachlorodibenzofuran
HxCDD – hexachlorodibenzo-p-dioxin
HxCDF – hexachlorodibenzofuran
LMCL – lower method calibration limit
OCDD – octachlorodibenzo-p-dioxin
OCDF – octachlorodibenzofuran
PeCDD – pentachlorodibenzo-p-dioxin
PeCDF – pentachlorodibenzofuran
RL – reporting limit
TCDD – tetrachlorodibenzo-p-dioxin
TCDF – tetrachlorodibenzofuran

Table 6. Surface water analytes, analytical methods, RL goals, and WQC

Analyte	Method	Unit	RL	National Recommended AWQC					Washington State Criteria[a]				
				Aquatic Life				Human Health	Aquatic Life				Human Health
				Freshwater		Marine			Freshwater		Marine		
				CMC (Acute)	CCC (Chronic)	CMC (Acute)	CCC (Chronic)	Consumption of Organism Only	Acute	Chronic	Acute	Chronic	Consumption of Organism Only
Metals and organometals													
Aluminum	EPA 1638	µg/L	20	750	87								
Antimony	EPA 1638	µg/L	0.3					640					90
Arsenic	EPA 1638	µg/L	0.4	340[b,c]	150[b,c]	69[b]	36[b]	0.14	360[b]	190[b]	69[b]	36[b]	0.14
Inorganic arsenic	EPA 1632	µg/L	0.025										0.14
Cadmium	EPA 1638	µg/L	0.12	1.8[b,c]	0.72[b,c]	33[b]	7.9[b]		3.7[b,c]	1[b,c]	42[b]	9.3[b]	
Chromium	EPA 1638	µg/L	0.75										
Chromium III[d]	na	µg/L		570[b,c]	74[b,c]				550	180			
Chromium VI[d]	na	µg/L		16[b c]	11[b,c]	1,100[b]	50[b]		15[b]	10[b]	1,100[b]	50	
Copper	EPA 1638	µg/L	0.66			4.8[b]	3.1[b]		17[b,c]	11[b,c]	4.8[b]	3.1[b]	
Iron	EPA 1638	µg/L	8.5		1,000								
Lead	EPA 1638	µg/L	0.15	65[b,c]	2.5[b,c]	210[b]	8.1[b]		65[b,c]	2.5[b,c]	210.0[b]	8.1[b]	
Manganese	EPA 1638	µg/L	0.63					100					
Mercury	EPA 1631E	µg/L	0.0004	1.4[b]	0.77[b]	1.8[b]	0.94[b]		2.1[b]	0.012[b]	1.8[b]	0.025[b]	
Methylmercury[d]	na	µg/L	0.05	1.4[b]	0.77[b]	1.8[b]	0.94[b]						
Nickel	EPA 1638	µg/L	0.69	470[b,c]	52[b,c]	74[b]	8.2[b]	4,600	1,400[b,c]	160[b,c]	74.0[b]	8.2[b]	100
Selenium	EPA 1638	µg/L	0.4			290	71	4,200	20	5	290[b]	71[b]	200
Silver	EPA 1638	µg/L	0.18	3.2[b,c]		1.9[b]			3.5[b,c]		1.9[b]		
Thallium	EPA 1638	µg/L	0.4					0.47					6.3
Zinc	EPA 1638	µg/L	4	120[b,c]	120[b,c]	90[b]	81[b]	26,000	110[b,c]	100[b,c]	90[b]	81[b]	
TBT	EPA 8270D-SIM	µg/L	**0.052**	0.46	0.072	0.42	0.0074						
PAHs													
Acenaphthene	EPA 8270D-SIM	µg/L	0.0100					90					30
Anthracene	EPA 8270D-SIM	µg/L	0.0100					400					100
Benzo(a)anthracene	EPA 8270D-SIM	µg/L	**0.0100**					0.0013					0.00016
Benzo(a)pyrene	EPA 8270D-SIM	µg/L	**0.0100**					0.00013					0.000016
Benzo(b)fluoranthene	EPA 8270D-SIM	µg/L	**0.0100**					0.0013					0.00016
Benzo(k)fluoranthene	EPA 8270D-SIM	µg/L	**0.0100**					0.013					0.0016
Chrysene	EPA 8270D-SIM	µg/L	0.0100					0.13					0.016
Dibenzo(a,h)anthracene	EPA 8270D-SIM	µg/L	**0.0100**					0.00013					0.000016
Fluoranthene	EPA 8270D-SIM	µg/L	0.0100					20					6
Fluorene	EPA 8270D-SIM	µg/L	0.0100					70					10

Table 6. Surface water analytes, analytical methods, RL goals, and WQC

Analyte	Method	Unit	RL	National Recommended AWQC					Washington State Criteria[a]				
				Aquatic Life				Human Health	Aquatic Life				Human Health
				Freshwater		Marine			Freshwater		Marine		
				CMC (Acute)	CCC (Chronic)	CMC (Acute)	CCC (Chronic)	Consumption of Organism Only	Acute	Chronic	Acute	Chronic	Consumption of Organism Only
Indeno(1,2,3-cd)pyrene	EPA 8270D-SIM	µg/L	**0.0100**					0.0013					0.00016
Pyrene	EPA 8270D-SIM	µg/L	0.0100					30					8
Phthalates													
Bis(2-ethylhexyl)phthalate	EPA 8270D	µg/L	**3.00**					0.37					0.046
Butyl benzyl phthalate	EPA 8270D	µg/L	**1.00**					0.1					0.013
Diethyl phthalate	EPA 8270D	µg/L	1.00					600					200
Dimethyl phthalate	EPA 8270D	µg/L	1.00					2,000					600
Di-n-butyl phthalate	EPA 8270D	µg/L	1.00					30					8
Other SVOCs													
1,2,4,5-Tetrachloro-benzene	EPA 8270D	µg/L	**1.00**					0.03					
1,2-Diphenylhydrazine	EPA 8270D	µg/L	**1.00**					0.2					0.02
2,4,5-Trichlorophenol	EPA 8270D	µg/L	5.00					600					
2,4,6-Trichlorophenol	EPA 8270D	µg/L	**3.00**					2.8					0.28
2,4-Dichlorophenol	EPA 8270D	µg/L	3.00					60					10
2,4-Dimethylphenol	EPA 8270D	µg/L	3.00					3,000					97
2,4-Dinitrophenol	EPA 8270D	µg/L	20.0					300					100
2,4-Dinitrotoluene	EPA 8270D	µg/L	**3.00**					1.7					0.18
2-Chloronaphthalene	EPA 8270D	µg/L	20.0					1000					100
2-Chlorophenol	EPA 8270D	µg/L	20.0					800					17
3,3'-Dichlorobenzidine	EPA 8270D	µg/L	**5.00**					0.15					0.0033
4,6-Dinitro-o-cresol	EPA 8270D	µg/L	**10.0**					30					7
4-Chloro-3-methylphenol	EPA 8270D	µg/L	3.00					2,000					36
Benzidine	EPA 8270D	µg/L	**10.0**					0.011					0.000023
bis(2-chloroethyl)ether	EPA 8270D	µg/L	**1.00**					2.2					0.06
bis(2-chloroisopropyl)ether	EPA 8270D	µg/L	0.241					4,000					900
bis(chloromethyl) ether	EPA 8270D	µg/L	**1.00[e]**					0.017					
Hexachlorobenzene	EPA 8270D	µg/L	**1.00**					0.000079					0.0000050
Hexachloroethane	EPA 8270D	µg/L	**2.00**					0.1					0.02
Hexachlorocyclopentadiene	EPA 8270D	µg/L	**5.00**					4					1
Isophorone	EPA 8270D	µg/L	1.00					1,800					110
N-Nitrosodiethylamine	EPA 8270D	µg/L	1.00[e]					1.24					
n-Nitrosodimethylamine	EPA 8270D	µg/L	**3.00**					3					0.34

Table 6. Surface water analytes, analytical methods, RL goals, and WQC

Analyte	Method	Unit	RL	National Recommended AWQC					Washington State Criteria[a]				
				Aquatic Life				Human Health	Aquatic Life				Human Health
				Freshwater		Marine			Freshwater		Marine		
				CMC (Acute)	CCC (Chronic)	CMC (Acute)	CCC (Chronic)	Consumption of Organism Only	Acute	Chronic	Acute	Chronic	Consumption of Organism Only
N-Nitroso-di-n-butylamine	EPA 8270D	µg/L	**1.00[e]**					0.22					
n-Nitroso-di-n-propylamine	EPA 8270D	µg/L	**1.0**					0.51					0.058
n-Nitrosodiphenylamine	EPA 8270D	µg/L	**1.00**					6					0.69
N-Nitrosopyrrolidine	EPA 8270D	µg/L	1.00[e]					34					
Nitrobenzene	EPA 8270D	µg/L	1.00					600					100
Nonylphenol (mixed isomers)	EPA 8270D	µg/L	1.00[e]	28	6.6	7	1.7						
Pentachlorobenzene	EPA 8270D	µg/L	**1.00[e]**					0.1					
Pentachlorophenol	EPA 8270D	µg/L	**10.0**	19	15	13	7.9	0.04	15[f]	9.5[f]	13	7.9	0.002
Phenol	EPA 8270D	µg/L	1.00					300,000					70,000
Total dinitrophenols	EPA 8270D	µg/L	3.0[e]					1000					
Total nitrosamines	EPA 8270D	µg/L	**20.0**					1.24					
PCBs													
Total PCB (congeners)	EPA 1668C	µg/L	0.00004[g]		0.014		0.03	0.000064	2	0.014	10	0.030	
Dioxins/furans													
2,3,7,8-TCDD	EPA 1613B	pg/L	**2.0**					5.1					0.014
Pesticides													
Parathion	EPA 8270D-SIM	µg/L	**0.20**	0.065	0.013				0.065	0.013			
4,4'-DDD	EPA 8081B	µg/L	**0.0500**					0.00012					0.0000079
4,4'-DDE	EPA 8081B	µg/L	**0.0500**					0.000018					0.00000088
4,4'-DDT	EPA 8081B	µg/L	**0.0500**	1.1	0.001	0.13	0.001	0.00003	1.1	0.001	0.13	0.001	0.0000012
Aldrin	EPA 8081B	µg/L	**0.0250**	3		1.3		0.00000077	2.5[h]	0.0019[h]	0.71[h]	0.0019[h]	0.000000041
Dieldrin	EPA 8081B	µg/L	**0.0500**	0.24	0.056	0.71	0.0019	0.0000012	2.5[h]	0.0019[h]	0.71[h]	0.0019[h]	0.000000070
alpha-BHC	EPA 8081B	µg/L	**0.0250**					0.00039					0.000048
beta-BHC	EPA 8081B	µg/L	**0.0250**					0.014					0.0014
gamma-BHC	EPA 8081B	µg/L	0.0250	0.95		0.16		4.4	2	0.08	0.16		0.43
Total chlordane	EPA 8081B	µg/L	**0.050**	2.4	0.0043	0.09	0.004	0.00032	2.4	0.0043	0.09	0.004	0.000022
alpha-Endosulfan	EPA 8081B	µg/L	**0.0250**	0.22[h]	0.056[h]	0.034[h]	0.0087[h]	30	0.22[i]	0.056[i]	0.034[i]	0.0087[i]	7
beta-Endosulfan	EPA 8081B	µg/L	**0.0250**	0.22[h]	0.056[h]	0.034[h]	0.0087[h]	40	0.22[i]	0.056[i]	0.034[i]	0.0087[i]	10
Endosulfan sulfate	EPA 8081B	µg/L	0.0500					40					10
Endrin	EPA 8081B	µg/L	**0.0500**	0.086	0.036	0.037	0.0023	0.03	0.18	0.0023	0.037	0.0023	0.002
Endrin aldehyde	EPA 8081B	µg/L	**0.0500**					1					0.035

Table 6. Surface water analytes, analytical methods, RL goals, and WQC

Analyte	Method	Unit	RL	National Recommended AWQC					Washington State Criteria[a]				
				Aquatic Life				Human Health	Aquatic Life				Human Health
				Freshwater		Marine			Freshwater		Marine		
				CMC (Acute)	CCC (Chronic)	CMC (Acute)	CCC (Chronic)	Consumption of Organism Only	Acute	Chronic	Acute	Chronic	Consumption of Organism Only
Heptachlor	EPA 8081B	µg/L	**0.0250**	0.52	0.0038	0.053	0.0036	0.0000059	0.52	0.0038	0.053	0.0036	0.00000034
Heptachlor epoxide	EPA 8081B	µg/L	**0.0500**	0.52	0.0038	0.053	0.0036	0.000032					0.0000024
Hexachlorocyclohexane-G	EPA 8081B	µg/L	**1.00[e]**					0.010					
Methoxychlor	EPA 8081B	µg/L	**0.250**		0.03		0.03	0.02					
Mirex	EPA 8081B	µg/L	**0.0500**		0.001		0.001						
Toxaphene	EPA 8081B	µg/L	**1.25**	0.73	0.0002	0.21	0.0002	0.00071	0.73	0.0002	0.21	0.0002	0.000032

Bold underlined reporting limits are greater than the lowest criteria value.

[a] Washington State criteria include standards promulgated in WAC 173-201A and human health criteria consistent with the NTR 40 CFR 131.36(b)(1) as applied to Washington 40 CFR 131(d)(14), including the 40 CFR 131 criteria updated on November 28, 2016.

[b] Criteria applied to dissolved fraction.

[c] Criteria based on hardness of 100 mg/L as calcium carbonate..

[d] Total value will be compared to criterion for related chemical species.

[e] Estimated RL; laboratory will confirm RL prior to analysis..

[f] Criteria based on pH of 7.5.

[g] Value represents laboratory-specific LMCL value for an individual PCB congener based on a 1-L sample.

[h] Criteria for sum of aldrin and dieldrin.

[i] Criteria for sum of alpha-Endosulfan and beta-Endosulfan.

AWQC – ambient water quality criteria
BHC – benzene hexachloride
CCC – criterion continuous concentration
CFR – Code of Federal Regulations
CMC – criterion maximum concentrations
DDD – dichlorodiphenyldichloroethane
DDE – dichlorodiphenyldichloroethylene
DDT – dichlorodiphenyltrichloroethane
EPA – US Environmental Protection Agency
LMCL – lower method calibration limit
na – not applicable
NTR – National Toxics Rule
PAH – polycyclic aromatic hydrocarbon
PCB – polychlorinated biphenyl
RL – reporting limit
SIM – selective ion monitoring
SVOC – semivolatile organic compound
TBT – tributyltin
TCDD – tetrachlorodibenzo-*p*-dioxin
WAC – Washington Administrative Code
WQC – water quality criteria

APPENDIX C. DATA MANAGEMENT PLAN

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Acronyms

AET	apparent effects threshold
AOC	Administrative Order on Consent
cPAH	carcinogenic polycyclic aromatic hydrocarbon
CSL	cleanup screening level
DDD	dichlorodiphenyldichloroethane
DDE	dichlorodiphenyldichloroethylene
DDT	dichlorodiphenyltrichloroethane
EPA	US Environmental Protection Agency
HPAH	high-molecular-weight polycyclic aromatic hydrocarbon
HpCDD	heptachlorodibenzo-*p*-dioxin
HpCDF	heptachlorodibenzofuran
HxCDD	hexachlorodibenzo-*p*-dioxin
HxCDF	hexachlorodibenzofuran
LAET	lowest apparent effects threshold
LDW	Lower Duwamish Waterway
LPAH	low-molecular-weight polycyclic aromatic hydrocarbon
OCDD	octachlorodibenzo-*p*-dioxin
OCDF	octachlorodibenzofuran
PAH	polycyclic aromatic hydrocarbon
PCB	polychlorinated biphenyl
PeCDD	pentachlorodibenzo-*p*-dioxin
PeCDF	pentachlorodibenzofuran
PEF	potency equivalency factor
QC	quality control
RI/FS	remedial investigation / feasibility study
RL	reporting limit
SCO	sediment cleanup objective
SIM	selected ion monitoring
SMS	Washington State Sediment Management Standards
SQS	sediment quality standards

SVOC	semivolatile organic compound
TCDD	tetrachlorodibenzo-*p*-dioxin
TCDF	tetrachlorodibenzofuran
TEF	toxic equivalency factor
TEQ	toxic equivalent
TOC	total organic carbon
WAC	Washington Administrative Code
WHO	World Health Organization

1 Introduction

This appendix presents the data management plan for the pre-design studies project. It contains two main sections:

- Section 2. Project database structure and data usability
- Section 3. Data management rules

2 Project Database Structure and Data Usability

The project database published with the Lower Duwamish Waterway (LDW) remedial investigation/feasibility study (RI/FS) is a Microsoft Access® database containing sediment, water, and tissue chemistry data for samples collected between 1990 and 2010. This section describes planned revisions to the project database structure; the incorporation of new in-waterway, upstream, and source control-related data compiled under Task 2;[1] and the process for future data additions.

2.1 Project Database Structure Revisions

The existing project database stores the RI/FS chemistry data in six media-specific tables: surface sediment, subsurface sediment, tissue, surface water, porewater, and seeps. In order to simplify usage and management of these data, the existing six tables will be consolidated into three tables containing in-waterway data of similar media types: sediment chemistry, tissue chemistry, and water chemistry.

The surface sediment and porewater tables in the existing project database are provided in two forms: one that includes field replicates as discrete samples ("sample-averaged"), and one that provides the average concentration of the parent and field replicate sample for each chemical ("location-averaged"). In order to reduce redundancy and simplify usage of these data, the updated database will present all data on a sample-averaged basis, with field replicates included as discrete samples and clearly identified.

2.2 Incorporation of Task 2 Data

The data compiled under Task 2 includes in-waterway, upstream, and source control-related samples collected between 2010 and 2016. These in-waterway data will be incorporated into the sediment, tissue, and water tables, as described in Section 2.1. The upstream and source control-related data will be added to the project database as five new tables: storm drain and combined sewer system source tracing solids, bank soils, groundwater, upstream surface water, and upstream suspended solids.

[1] Task 2 of the pre-design studies outlined in the third amendment to the Administrative Order on Consent (AOC) (EPA 2016).

2.3 DATA ADDITIONS

Chemistry data from each pre-design study sampling event will be incorporated into the project database following receipt of validated data. In addition, as appropriate, additional in-waterway data unrelated to the pre-design studies will be added as they are made available.

New data will be incorporated into the media-specific tables described in Sections 2.1 and 2.2. Prior to incorporating these data into the database, the new data will be assessed for quality and usability using the data quality review process described in the Task 2 data compilation memo (Windward and Integral 2017).

Additions and revisions to the project database will be documented in a change log table within the Microsoft Access® database. A list of all data additions following the Task 2 compilation will be included in Task 6, the data evaluation report. A final version of the Microsoft Access® project database will be submitted to the US Environmental Protection Agency (EPA) at the end of the project.

2.4 DATA USABILITY

Although the RI/FS and data compiled under Task 2 will be combined for ease of use, these two datasets were originally compiled using different approaches, and the following caveats should be considered during use:

- Preparation of the RI/FS dataset included a spatial and temporal evaluation process that allowed newer data to override older co-located results. This process was conducted for the RI/FS dataset to show the most recent results. No equivalent process was applied to the Task 2 dataset.
- The compilation work for Task 2 specifically excluded pre-cleanup surface and subsurface sediment data from areas that have been dredged or otherwise remediated, so the dataset does not represent all in-waterway data collected between 2010 and 2016.
- The updated in-waterway sediment table will provide a comparison to current Washington State Sediment Management Standards (SMS) criteria, as appropriate. These criteria have been revised since the RI/FS dataset was originally published,[2] so the screening outcomes will not match those previously reported.
- In the RI/FS surface sediment dataset, a single averaged concentration was reported for each chemical at locations that had a field replicate sample. In merged RI/FS and Task 2 datasets for sediment, both parent and field replicate

[2] Some dry weight apparent effects thresholds (AETs) have changed, as well as the total organic carbon (TOC) threshold for carbon normalization.

results for each location will be provided; maps will present the parent sample result instead of an average.

These data usability considerations will be noted in a reference table in the project database, and the data source for each sample (e.g. RI/FS, Task 2) will be clearly identified in each of the chemistry tables.

3 Data Management Rules

Data management rules being followed for the pre-design studies are the same as those applied to the RI/FS dataset, except as noted in this section. Rules summarized in this appendix include those for averaging duplicate or replicate samples (Section 3.1), selecting the preferred result if more than one result is reported for a chemical (Section 3.2), handling significant figures and rounding (Section 3.3), calculating totals when results are summed for individual components (Section 3.4), calculating toxic equivalents (TEQs) for polychlorinated biphenyl (PCB) congeners and dioxin/furan congeners (Sections 3.5 and 3.6, respectively), and calculating carcinogenic polycyclic aromatic hydrocarbons (cPAHs) (Section 3.7).

3.1 Averaging Laboratory Duplicate or Replicate Samples

Contaminant concentrations obtained from the analysis of laboratory duplicates or replicates (i.e., two or more analyses on the same sample) will be averaged for a closer representation of the "true" concentration than that provided by the results of a single analysis. Averaging rules will be dependent on whether the individual results are detected concentrations or reporting limits (RLs) for non-detected analytes. If all concentrations are detected for a given parameter, the values will be simply averaged arithmetically. If all concentrations are non-detected for a given parameter, the minimum RL will be reported. If the concentrations are a mixture of detected concentrations and RLs, any two or more detected concentrations will be averaged arithmetically, and RLs will be ignored. If there is one detected concentration and one or more RLs, the detected concentration will be reported. The latter two rules will be applied regardless of whether the RLs are higher or lower than the detected concentration.

3.2 Selection of Preferred Results

In some instances, the laboratory will generate more than one result for a chemical for a given sample. Multiple results can occur for several reasons, including:

- The original result does not meet the laboratory's internal quality control (QC) guidelines, and a reanalysis is performed.
- The original result does not meet other project data quality objectives, such as a sufficiently low RL, and a reanalysis is performed.

- Two different analytical methods are used for that chemical.

In each case, a single result will be selected for use. The procedures for selecting the preferred result will differ depending on whether a single or multiple analytical methods are used for that chemical.

For the same analytical method, the results will be selected using the following guidance:

- If the results are detected and not qualified, then the result from the lowest dilution will be selected, unless multiple results from the same dilution are available, in which case the result with the highest concentration will be selected.
- If the results are a combination of estimated and unqualified detected results, then the unqualified result will be selected. This situation most commonly occurs when the original result is outside of the calibration range, thus requiring a dilution. The diluted result within the calibration range will be preferentially selected.
- If the results are all estimated, then the ~~preferred~~ result will be selected using best professional judgment and considering the rationale for qualification. For example, a result qualified based on laboratory replicate results outside of QC objectives for precision will be preferred to a qualified result that is outside the calibration range.
- If the results are a combination of detected and non-detected results, then the detected result will be selected. If there are more than one detected result, the applicable rules for multiple results (as discussed above) will be followed.
- If the results are all non-detected, then the lowest RL will be selected.

For different analytical methods (i.e., when a specific chemical is analyzed in the same sample using different methods), the following rules will be applied:

- For results analyzed using the semivolatile organic compound (SVOC) full-scan (EPA 8270) and selected ion monitoring (SIM) (EPA 8270-SIM) methods, the SIM results will be selected.
- For results analyzed using EPA Method 8081A and any 8270 method (i.e., hexachlorobenzene and hexachlorocyclopentadiene), the 8081A result will be selected.

The RI/FS database rules for the selection of preferred results between two methods (as described above) are revised for the compilation of the pre-design data. In the RI/FS, the preferred result was selected based on a comparison between the methods of the detection status, RL, and data qualifiers. The revised rules select the preferred result based on a preference for method.

3.3 SIGNIFICANT FIGURES AND ROUNDING

The analytical laboratories report results with various numbers of significant figures depending on the instrument, parameter, and concentration relative to the RL. The reported (or assessed) precision of each observation will be explicitly stored in the project database as a record of the number of significant figures assigned by the laboratory. The tracking of significant figures will become important when calculating averages and performing other data summaries.

When a calculation involves addition, such as totaling PCBs or polycyclic aromatic hydrocarbons (PAHs), the calculation will be only as precise as the least precise number that goes into the calculation. For example (assuming two significant figures):

> 210 + 19 = 229 will be reported as 230 because 19 is only reported to 2 significant digits, and the enhanced precision of the trailing 0 in the number 210 is not significant.

When a calculation involves multiplication or division, such as carbon normalization, the original figures for each value are carried through the calculation (i.e., individual values are not adjusted to a standard number of significant figures; instead, the appropriate adjustment is made to the resultant value at the end of the calculation). The result is rounded at the end of the calculation to reflect the value with the fewest significant figures used in the calculation. For example:

> 59.9 x 1.2 = 71.88 will be reported as 72 because there are 2 significant figures in the number 1.2.

When rounding, if the number following the last significant figure is less than 5, the digit will be left unchanged. If the number following the last significant figure is equal to or greater than 5, the digit will be increased by 1.

3.4 CALCULATING TOTALS

Total PCBs, total dichlorodiphenyltrichloroethanes (DDTs), total PAHs, total chlordane, total xylenes, and total nitrosamines will be calculated by summing the detected values for the individual components (e.g., Aroclor mixtures or individual congeners for total PCBs). For samples in which none of the individual components are detected, the total value will be given as the highest RL of any individual component, and assigned a U-qualifier (no detected concentrations). No sum will be calculated in ~~In~~ cases where 50% or less of the ~~sum~~ components are analytes~~, no sum will be calculated~~. Concentrations for analyte sums will be calculated using the following components:

- Total PCBs will be calculated, in accordance with the methods of the SMS, using only detected values for all Aroclor mixtures. For individual samples in which none of the Aroclor mixtures are detected, total PCBs will be given a

value equal to the highest RL of the Aroclors and assigned a U-qualifier (no detected concentrations).

- Total low-molecular-weight PAHs (LPAHs), high-molecular-weight PAHs (HPAHs), PAHs, and benzofluoranthenes will also be calculated in accordance with the methods of the SMS. Total LPAHs will be the sum of detected concentrations for naphthalene, acenaphthylene, acenaphthene, fluorene, phenanthrene, and anthracene. Total HPAHs were the sum of detected concentrations for fluoranthene, pyrene, benzo(a)anthracene, chrysene, total benzofluoranthenes, benzo(a)pyrene, indeno(1,2,3,-c,d)pyrene, dibenzo(a,h)anthracene, and benzo(g,h,i)perylene. Total benzofluoranthenes will be the sum of the b (i.e., benzo(b)fluoranthene), j, and k isomers.

  Because the j isomer is rarely quantified, the total benzofluoranthenes sum will be typically calculated with only the b and k isomers. In cases where the laboratory provides total benzofluoranthenes instead of or in addition to the b and k isomers, the laboratory result will be reported, and no sum will be calculated. For samples in which all individual compounds within any of the three groups described above are non-detected, the highest RL for that sample will represent the sum.

- Total DDTs will be calculated using only detected values for the DDT isomers: 2,4′-dichlorodiphenyldichloroethane (DDD); 4,4′-DDD; 2,4′-dichlorodiphenyldichloroethylene (DDE); 4,4′-DDE; 2,4′-DDT; and 4,4′-DDT. For individual samples in which none of the isomers are detected, total DDTs will be given a value equal to the highest RL of the six isomers and assigned a U-qualifier (no detected concentrations).

- Total chlordane will be calculated using only detected values for the following compounds: alpha-chlordane, gamma-chlordane, oxychlordane, cis-nonachlor, and trans-nonachlor. For individual samples in which none of these compounds are detected, total chlordane will be given a value equal to the highest RL of the five compounds listed and assigned a U-qualifier (no detected concentrations).

- Total xylene will be calculated using only detected values for m,p-xylene and o-xylene. For individual samples in which neither of these compounds are detected, total xylene will be given a value equal to the higher RL of the two compounds listed and assigned a U-qualifier (no detected concentrations).

- Total nitrosamines will be calculated using only detected values for n-nitrodiethylamine, n-nitrosodimethylamine, n-nitroso-di-n-butylamine, n-nitroso-di-n-propylamine, and n-nitrosodiphenylamine. For individual samples in which none of these compounds are detected, total nitrosamines will be given a value equal to the highest RL of the five compounds listed and assigned a U-qualifier (no detected concentrations).

3.5 CALCULATION OF PCB CONGENER TOXIC EQUIVALENTS

PCB congener TEQs will be calculated using the World Health Organization (WHO) consensus toxic equivalency factor (TEF) values for mammals (Van den Berg et al. 1998; Van den Berg et al. 2006), as presented in Table 1. The TEQ will be calculated as the sum of each PCB congener concentration multiplied by the corresponding TEF value. When the PCB congener concentration is reported as non-detected, then the TEF will be multiplied by one-half the RL.

Table 1. PCB congener TEF values

PCB Congener No.	TEF Value for Mammals (unitless)[a]
77	0.0001
81	0.0003
105	0.00003
114	0.00003
118	0.00003
123	0.00003
126	0.1
156	0.00003
157	0.00003
167	0.00003
169	0.03
189	0.00003

[a] From Van den Berg et al. (2006).
PCB – polychlorinated biphenyl
TEF – toxic equivalency factor

3.6 CALCULATION OF DIOXIN/FURAN CONGENER TEQS

Dioxin/furan congener TEQs will be calculated using the WHO consensus TEF values for mammals (Van den Berg et al. 1998; Van den Berg et al. 2006) as presented in Table 2. The TEQ will be calculated as the sum of each dioxin/furan congener concentration multiplied by the corresponding TEF value. When the dioxin/furan congener concentration is reported as non-detected, then the TEF will be multiplied by one-half the RL.

Table 2. Dioxin/furan congener TEF values

Dioxin/Furan Congener	TEF Value for Mammals (unitless)[a]
1,2,3,4,6,7,8-HpCDF	0.01
1,2,3,4,6,7,8-HpCDD	0.01
1,2,3,4,7,8,9-HpCDF	0.01

Dioxin/Furan Congener	TEF Value for Mammals (unitless)[a]
1,2,3,4,7,8-HxCDF	0.1
1,2,3,4,7,8-HxCDD	0.1
1,2,3,6,7,8-HxCDF	0.1
1,2,3,6,7,8-HxCDD	0.1
1,2,3,7,8,9-HxCDF	0.1
1,2,3,7,8,9-HxCDD	0.1
1,2,3,7,8-PeCDF	0.03
1,2,3,7,8-PeCDD	1
2,3,4,6,7,8-HxCDF	0.1
2,3,4,7,8-PeCDF	0.3
2,3,7,8-TCDF	0.1
2,3,7,8-TCDD	1
OCDF	0.0003
OCDD	0.0003

[a] From Van den Berg et al. (2006).

HpCDD – heptachlorodibenzo-*p*-dioxin
HpCDF – heptachlorodibenzofuran
HxCDD – hexachlorodibenzo-*p*-dioxin
HxCDF – hexachlorodibenzofuran
OCDD – octachlorodibenzo-*p*-dioxin
OCDF – octachlorodibenzofuran
PeCDD – pentachlorodibenzo-*p*-dioxin
PeCDF – pentachlorodibenzofuran
TCDD – tetrachlorodibenzo-*p*-dioxin
TCDF – tetrachlorodibenzofuran
TEF – toxic equivalency factor

3.7 Calculation of Carcinogenic Polycyclic Aromatic Hydrocarbons

cPAH values will be calculated using potency equivalency factor (PEF) values (California EPA 2009) based on the individual PAH component's relative toxicity to benzo(a)pyrene. PEF values are presented in Table 3. The cPAH will be calculated as the sum of each individual PAH concentration multiplied by the corresponding PEF value. When the individual PAH component concentration are reported as non-detected, then the PEF will be multiplied by one-half the RL.

Table 3. cPAH PEF values

cPAH	PEF Value (unitless)[a]
Benzo(a)pyrene	1
Benzo(a)anthracene	0.1
Benzo(b)fluoranthene	0.1
Benzo(k)fluoranthene	0.1
Chrysene	0.01
Dibenz(a,h)anthracene	0.4
Indeno(1,2,3-cd)pyrene	0.1

[a] PEFs for cPAHs are defined by California EPA (2009) by dividing the inhalation unit risk factor for the compound by the inhalation unit risk factor for benzo[a]pyrene.

cPAH – carcinogenic polycyclic aromatic hydrocarbon

EPA – US Environmental Protection Agency

PEF – potency equivalency factor

3.8 TOC NORMALIZATION

For comparison to benthic cleanup goals, sediment samples with TOC content < 0.5% or > 3.5% will not be TOC normalized for comparison to the organic carbon-normalized RALs and SMS criteria (Ecology 2015). When TOC normalization is not possible and the dry weight concentration is greater than lowest apparent effects threshold (LAET) and less than or equal to 2LAET, the concentration will be considered to be greater than sediment cleanup objectives (SCOs)[3] and less than or equal to the cleanup screening level (CSL).

[3] SCO, as defined in the 2013 SMS Rule (Washington Administrative Code [WAC] 173-204-562), is equivalent to the term sediment quality standard (SQS) used in the RI/FS (Windward 2010; AECOM 2012).

3.9 CALCULATION OF RECONSTITUTED WHOLE-BODY TISSUE FOR CRAB AND CLAMS

Reconstituted whole-body crab tissue concentrations will be calculated using Equation 1:

$$C_{WB} = \left(C_{hepatopancreas} \times f_{hepatopancreas}\right) + \left(C_{ediblemeat} \times f_{ediblemeat}\right) \qquad \textbf{Equation 1}$$

Where:

C_{WB}	=	estimated whole-body tissue concentration (mg/kg ww)
$C_{hepatopancreas}$	=	hepatopancreas tissue concentration (mg/kg ww)
$F_{hepatopancreas}$	=	average fraction of whole-body weight that is hepatopancreas (average hepatopancreas weight fraction of individual crab that are included in composite sample)
$C_{edible\ meat}$	=	edible meat concentration (mg/kg ww)
$F_{edible\ meat}$	=	average fraction of whole-body weight that is edible meat (average edible meat fraction of individual crab that are included in composite sample)

Reconstituted whole-body clam tissue concentrations will be calculated using Equation 2:

$$C_{WB} = \left(C_{siphonskin} \times f_{siphonskin}\right) + \left(C_{remainder} \times f_{remainder}\right) \qquad \textbf{Equation 2}$$

Where:

C_{WB}	=	estimated whole-body tissue concentration (mg/kg ww)
C_{siphon}	=	siphon skin tissue concentration (mg/kg ww)
F_{siphon}	=	average fraction of whole-body weight that is siphon skin (average siphon skin weight fraction of individual clams that are included in composite sample)
$C_{remainder}$	=	remaining body concentration (mg/kg ww)
$F_{remainder}$	=	average fraction of whole-body weight that is the remaining body (average remaining body fraction of individual clams that are included in composite sample)

For reconstituted whole-body concentrations that include a non-detected value for at least one tissue type composite, the non-detected value(s) will be represented in the calculation by one-half the detection limit; the final reconstituted whole-body result will be treated as a detected result. In cases where all tissue type composites are non-detected values, the final reconstituted whole-body result will be assigned a U-qualifier (no detected results), and the weighted sum of the detection limits for the two components will be used to represent the non-detected whole-body concentration.

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APPENDIX D. SUMMARY OF REMEDIAL DESIGN DATA NEEDS AND TIMING

No.	Data Need	Data Collection Activities	Timing Considerations	2015-2019 ENR/AC Pilot Study	2016-2019 Pre-Design Studies	TBD[a] Remedial Design Investigation[b]	TBD[a] Remedial Design Engineering[b,c]	TBD[a] Remedial Action[d]
Environmental Concerns								
1	Characterize surface sediment baseline conditions to: · Serve as a baseline for comparison to post-remedial action data. · Evaluate post-RI/FS trends reflecting the combined effects of EAAs, source control progress, and natural recovery processes	Sampling and analysis of COCs in: · Site-wide sediment (0–10 cm) SWAC and 95UCL · Site-wide clamming area intertidal sediment (0–45 cm) mean and 95UCL · Individual beach play areas sediment (0–45 cm) means and 95UCL	After early actions to establish baseline conditions for RAOs 1, 2, and 4		ü			
2	Characterize tissue baseline conditions to: · Serve as a baseline for comparison to post-remedial action data · Evaluate post-RI/FS trends reflecting the combined effects of EAAs, source control progress, and natural recovery processes.	Sampling and analysis of COCs in fish, crab, and clam tissues	2+ years after last early action to establish baseline conditions for tracking progress toward target tissue levels associated with RAO 1		ü			
3	Characterize surface water baseline conditions to: · Serve as a baseline for comparison to post-remedial action data · Evaluate post-RI/FS trends reflecting the combined effects of EAAs, source control progress, and natural recovery processes.	Sampling and analysis of water quality criteria parameters in surface water	After early actions to establish baseline conditions and facilitate assessment of progress toward ARAR compliance		ü			
4	Evaluate need for additional data for porewater baseline conditions for RAO 1 risk drivers, and evaluate need for additional data to further understand possible arsenic and cPAH concentrations in clam tissue following remediation.	Evaluate need for sediment porewater for human health risk drivers in ENR/MNR areas and arsenic and cPAHs in clamming areas.	Prior to remedial action and after evaluation of RARE, MIT, and baseline ENR/AC pilot study data are available; studies, if needed, would best be accomplished before remedial action to avoid confounding effects of dredging on tissue	ü	if needed[e]			
5	Characterize COCs in sediment to support delineation of remedial technology assignment boundaries, definition of dredge prisms, and waste characterization.	Location-specific sampling and analysis of COCs in sediments, including: · Limits of surface (0–10 cm) and subsurface (0–45 or 0–60 cm) RAL exceedances · Subsurface coring to determine dredge prisms and characterize waste · Characterization of surface (0–10 cm) COC trends to support revised estimates of sedimentation and recovery for MNR > SCO areas	Data must be obtained during design to finalize technology assignments, establish accurate delineation of remedial technology footprints, and design dredge prisms.			ü		

No.	Data Need	Data Collection Activities	Timing Considerations	2015-2019 ENR/AC Pilot Study	2016-2019 Pre-Design Studies	TBD[a] Remedial Design Investigation[b]	TBD[a] Remedial Design Engineering[b,c]	TBD[a] Remedial Action[d]
6	Characterize COCs in sediment porewater to support: · ENR with *in situ* treatment (AC) added · Cap design[f]	For *in situ* treatment, ENR/AC pilot study bulk sediment and porewater PCB data For cap design, equilibrium partitioning calculations based on COCs in sediment Area-specific sampling of sediment porewater, if needed for unusual conditions	Decision for carbon amendment addition to ENR will be based on ENR/AC pilot study outcomes. Cap designs are generally based conservatively on equilibrium partitioning unless unique circumstances require porewater data. Porewater data, if needed, should be obtained during design investigation/design engineering phases based on cap limits and design objectives.	ü		ü	ü	
7	Characterize COCs in relevant media to support source control sufficiency determinations	Sampling and analysis of COCs in: · LDW surface sediment near outfalls · Bank soils · Groundwater seeps	Implement early (i.e., pre-design), with supplemental information, as needed, during design.[f]		ü	ü		
Hydrogeological/Geotechnical								
8	Characterize groundwater upwelling rates to support cap design.[f]	Typically evaluate using existing hydrogeologic information or modeling to estimate groundwater upwelling velocities for purposes of cap design. Seepage meters may be used if more refined velocity estimates are needed.	Any new data needed should be obtained during design investigations based on cap limits and design objectives.			ü	ü	
9	Conduct area-specific characterization of sediment geotechnical properties to: · Determine sediment stability and stable side-slope requirements · Characterize sediment dredgeability · Support sediment consolidation assessment for cap design · Support selection of dredge equipment · Support design of sediment handling, transport, dewatering, treatment systems, and disposal requirements	Area-specific geotechnical sampling and analysis of sediments, including: · Geologic characterization · Sediment index properties · Sediment strength and consolidation properties	Data must be obtained during design investigation/design engineering phases to support accurate design and ensure safe and reliable performance of completed remedy. Certain data may be collected by remedial construction contractor to support design of sediment and dewatering processing systems.			ü	ü	ü
Geophysical/Physical								
10	Perform detailed geophysical characterization to: · Support accurate dredge, cap, and debris quantity estimates · Support dredge/cap prism design and evaluation of water depth constraints	Physical surveys: · Site-wide bathymetric and topographic surveys · Specialized surveys as appropriate for debris characterization (e.g., side-scan sonar, magnetometer, or sub-bottom profiling)	Data must be obtained during design investigation/design engineering to support accurate design.			ü	ü	

No.	Data Need	Data Collection Activities	Timing Considerations	2015-2019 ENR/AC Pilot Study	2016-2019 Pre-Design Studies	TBD[a] Remedial Design Investigation[b]	TBD[a] Remedial Design Engineering[b,c]	TBD[a] Remedial Action[d]
11	Obtain information regarding fixed structures to: · Assess constraints on future sampling activities, recovery categories, remedial technology assignments, and construction activities	Perform assessment and survey of in-water structures.	Perform early reconnaissance-level identification of all structures with the potential to influence recovery categories to inform future sampling and/or design analyses. Additional surveys/inspections of certain structures may also be performed during remedial design to support constructability and safety/stability analysis for dredging and capping activities. Remediation contractor will also perform pre-construction surveys to document structure conditions prior to construction.		ü	ü		ü
12	Physical/operational uses	Perform vessel/use survey.	Perform the vessel/use survey early to identify physical disturbances that may affect recovery categories, technology assignments, or design details. Review and update as needed during design investigation/design engineering.		ü	ü	ü	
13	Evaluate sediment transport and erosion/scour processes to support: · Delineation of MNR/ENR areas · Design of ENR/*in situ* treatment · Cap design · Outfall scour protection	Perform location-specific pilot testing and engineering analyses	The ENR/AC pilot study will provide information regarding the relative stability of AC with ENR The pre-design studies (waterway user survey and assessment of in-water structures) will provide information that can be used during design to inform development of parameters for evaluation of vessel-induced erosion/scour forces. During design, readily available hydrodynamic data[g] will be used to evaluate erosion/scour forces (due to river currents, vessels, outfall discharges, etc.) and associated stability of sediments, ENR/*in situ* treatment amendments, and cap materials.	ü	ü	ü	ü	
14	Perform an assessment to evaluate effect of designed remedial elements (e.g., sediment cap, riverbank armor) on water surface elevations, velocities, shear stress, and sediment mobility.[f]	Cross section analysis or hydrodynamic modeling	Assessment to be performed as needed during design using the configuration of the remedy as designed.				ü	

No.	Data Need	Data Collection Activities	Timing Considerations	2015-2019 ENR/AC Pilot Study	2016-2019 Pre-Design Studies	TBD[a] Remedial Design Investigation[b]	TBD[a] Remedial Design Engineering[b,c]	TBD[a] Remedial Action[d]
Implementation Planning/Other								
15[h]	Determine space requirements to establish construction support areas, including: · Transload facilities · Dredge material handling/stabilization areas · Construction water management/treatment · Laydown/material storage · Field office and support facilities	Identify space requirements and candidate sites.	Identify space and performance requirements to be performed in conjunction with remedial design to facilitate contractor bids. Identify specific properties and negotiation of access, lease, and/or purchase agreements to be performed by owners during engineering design or by the selected remedial contractor(s) during the remedial action.				ü	ü
16[h]	Haul routes	Identify transportation routes for truck/rail/barge transport of materials.	Identify minimum requirements in design with details developed in contractor's remedial action work plan.				ü	ü
17[h]	Determine current and reasonably anticipated future uses that may influence sampling design, recovery categories, technology assignments, delineation of remedial boundaries, and institutional controls.	Identify and document known or reasonably anticipated future waterway-dependent uses with potential to disturb sediment bed.	Determine uses early (i.e., pre-remedial design) to inform location-specific remedial design activities. Refine and verify information during design investigation/design engineering.		ü	ü	ü	
18[h]	Establish logistic or design details to accommodate waterway users that may be affected by remedial construction activities (e.g., Tribes, recreational users, facility operators, bridge operators, etc.).	Identify waterway users that may be affected by remedial construction activities. Collect information that may be used in coordinating access and/or temporary restrictions. Task includes development of vessel management plans and coordination with waterfront operators, recreational users, and tribal fishing representatives.	Pre-design investigation user survey (noted above) will be updated and refined throughout remedial design/remedial action phases to ensure the information is useful and current.		ü	ü	ü	ü
19[h]	Identify in-river and shoreline areas with cultural and archaeological resources and determine needed offsets for dredge/cap areas.	Establish area-specific delineation of archaeologically or culturally sensitive areas.	Identify areas during design, following establishment of dredge and capping limits, to facilitate coordination of any needed adjustments.			ü	ü	
20	Identify potential backfill and reactive amendment material sources.	Develop acceptance criteria; research and compile locally available sources and data.	Conduct preliminary identification of potential sources as part of remedial design, in conjunction with development of specifications. Remediation contractor will perform final identification/selection.				ü	ü
21	Perform bench-scale/treatability testing to support water treatment. [f]	Perform bench-scale tests, as-needed: · Column settling · Water treatability	Perform tests during remedial design, if needed based on dredging and water management requirements developed in design.				ü	

[a] The timing of remedial design and remedial action will be evaluated as part of Task 10 of the pre-design studies.

[b] New remedial design field measurements (e.g., sampling, surveying) are primarily accomplished during "Remedial Design Investigation."

[c] "Remedial design engineering" includes agency, owner/operator, and stakeholder reviews and input on design packages (e.g., 30%, 60%, 90%, Final) with increasing development of details. Additional data needs are commonly identified during early design phases as design elements mature. Limited field studies may be needed during the design engineering phase to support final design details.

[d] Remedial action includes development of remedial action work plan with specific means and methods proposed by the contractor. Remedial action work plan includes agency, owner/operator, and stakeholder reviews/input.

[e] The porewater addendum to the pre-design studies work plan will present an evaluation of available RARE, MIT, and baseline ENR/AC pilot study data and determine what, if any, supplemental porewater sampling may be required to address this need.

[f] The need for these data will be confirmed during remedial design engineering based on design approaches and evaluation of existing data.
[g] Data collection and/or input parameterization will consider potential influence of regional climate change and associated long-term resiliency of the remedy.
[h] These elements will also be informed by community and stakeholder input during the design.

AC – activated carbon
ARAR – applicable or relevant and appropriate requirement
COC – contaminant of concern
ENR – enhanced natural recovery
LDW – Lower Duwamish Waterway
MIT – Massachusetts Institute of Technology
MNR – monitored natural recovery
RAL – remedial action level
RARE – Regional Applied Research Effort
SCO – sediment cleanup objective
95UCL – 95% upper confidence limit for the mean